

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: November 21, 2002, 13:40:47 ; Search time 11 Seconds  
(without alignments)  
203.611 Million cell updates/sec

Title: US-09-776-724A-142

Perfect score: 283

Sequence: 1 MRRCVHVLGILVKNLY.....FQEAFLFFLLKNPLTCS 54

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	60	21.2	111	1 YG2C_YEAST	P53245 saccharomyc
2	59	20.8	310	1 O2A4_HUMAN	O95047 homo sapien
3	56.5	20.0	153	1 YG64_YEAST	P53342 saccharomyc
4	56.5	20.0	399	1 TRPB_BUCAP	P42391 buchnera ap
5	56	19.8	378	1 CKR7_MOUSE	P47774 mus musculu
6	55.5	19.6	363	1 YRU5_CAEEL	O09351 caenorhabdi
7	55.5	19.6	385	1 MDOC_ECOLI	P75920 escherichia
8	54.5	19.3	596	1 MKC7_YEAST	P53379 saccharomyc
9	54	19.1	633	1 YIJ2_YEAST	P40497 saccharomyc
10	53	18.7	230	1 UL16_HCMVA	P16757 human cytom
11	53	18.7	265	1 AQP5_HUMAN	P55064 homo sapien
12	53	18.7	322	1 CGM2_SCHPO	P36613 schizosacch
13	53	18.7	386	1 ADT1_GOSHI	O22342 gossypium h
14	53	18.7	643	1 VP4B_VACCV	P06440 vaccinia vi
15	53	18.7	644	1 VP4B_VACCC	P20643 vaccinia vi
16	52.5	18.6	350	1 OSTG_YEAST	P48439 saccharomyc
17	52.5	18.6	492	1 TR11_FUSSP	O13317 fusarium sp
18	52.5	18.6	716	1 IKKE_HUMAN	O14164 homo sapien
19	52.5	18.6	2670	1 YAO5_SCHPO	O10105 schizosacch
20	52	18.4	337	1 PAHX_BOVIN	O18778 bos taurus
21	52	18.4	378	1 CKR7_HUMAN	P32248 homo sapien
22	52	18.4	487	1 C135_DROME	O9vgb5 drosophila
23	52	18.4	644	1 VP4B_VARV	P33818 variola vir
24	52	18.4	677	1 NCPR_CAVPO	P37039 cavia porce
25	52	18.4	692	1 PHSG_AQUAE	O66932 aquifex aeo
26	51.5	18.2	124	1 MUTT_BUCAI	P57298 buchnera ap
27	51.5	18.2	318	1 YNN2_YEAST	P18239 saccharomyc
28	51.5	18.2	1056	1 YNN2_YEAST	P53914 saccharomyc
29	51	18.0	367	1 YQL2_CAEEL	O09291 caenorhabdi
30	51	18.0	1122	1 PHVA_ARATH	P14712 arabidopsis
31	51	18.0	1262	1 CYA5_RAT	O04400 rattus norv
32	51	18.0	1264	1 CYA5_RAT	P40144 oryctolagus
33	51	18.0	2524	1 NOTC_XENLA	P21783 xenopus lae

34	50.5	17.8	286	1 YTCP_BACSU	P53561 bacillus su
35	50.5	17.8	305	1 ADT_KLULA	P49382 kluyveromyc
36	50.5	17.8	397	1 TRPB_BUCDN	O68428 buchnera ap
37	50.5	17.8	523	1 PRIM_BORBU	O51653 borrelia bu
38	50.5	17.8	1071	1 UBP7_YEAST	P40453 saccharomyc
39	50	17.7	338	1 PAHX_HUMAN	O14832 homo sapien
40	50	17.7	396	1 ARRS_XENLA	P51477 xenopus lae
41	50	17.7	411	1 MKO8_RAT	P49185 rattus norv
42	50	17.7	427	1 MKO8_HUMAN	P45983 homo sapien
43	50	17.7	447	1 GNTF_ECOLI	P39373 escherichia
44	50	17.7	606	1 NUSM_FELCA	P48921 felis silve
45	50	17.7	676	1 NCPR_HUMAN	P16435 homo sapien

## ALIGNMENTS

RESULT 1			
YG2C_YEAST	STANDARD;	PRT;	111 AA.
ID P53245;			
DT 01-OCT-1996 (Rel. 34, Created)			
DT 01-OCT-1996 (Rel. 34, Last sequence update)			
DT 16-OCT-2001 (Rel. 40, Last annotation update)			
DE Hypothetical 13.6 kda protein in VHT1-ROM1 intergenic region.			
GN YGR069W.			
OS Saccharomyces cerevisiae (Baker's yeast).			
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;			
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.			
OX NCBI_TaxID=4932;			
RN [1]			
RP SEQUENCE FROM N.A.			
RA Wedler H., Scharfe M., Wedler E., Wambutt R.;			
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.			
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CC or send an email to license@sib-sib.ch).			
DR EMBL; Z72853; CAA97071.1; .			
DR SGD; S0003301; YGR069W.			
KW Hypothetical protein; Transmembrane.			
FT TRANSMEM 27 47 POTENTIAL.			
FT DOMAIN 36 47 POLY-PHE.			
SQ SEQUENCE 111 AA; 13603 MW; 161DE34E1D75AAEA CRC64;			
Query Match	21.2%;	Score 60;	DB 1; Length 111;
Best Local Similarity	34.0%;	Pred. No. 0.63;	
Matches 16;	Conservative 5;	Mismatches 20;	Indels 6; Gaps 1;
OY 4 CVRHLVGLIVLKNLYPHKNSMYPSPKLSLSSQEAFLFFLLIKNPL 50			
DB 12 CTRYEL-----LLPSYTHPNHLFHPSPISFFFFFFFFFFFRNCL 52			
RESULT 2			
O2A4_HUMAN	STANDARD;	PRT;	310 AA.
ID O2A4_HUMAN			
AC O95047;			
DT 16-OCT-2001 (Rel. 40, Created)			
DT 16-OCT-2001 (Rel. 40, Last sequence update)			
DT 16-OCT-2001 (Rel. 40, Last annotation update)			
DE Olfactory receptor 2A4.			
GN OR2A4.			
OS Homo sapiens (Human).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX NCBI_TaxID=9606;			
RN [1]			



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DR EMBL; Z19055; CAA79500.1; -.
DR HSP; P00933; 2WSY.
DR InterPro; IPR001926; B6_enzyme_beta.
DR InterPro; IPR000993; Trp_synth_beta.
DR Pfam; PF00291; PALP; 1.
DR TIGRFAMs; TIGR00263; trpB; 1.
DR PROSITE; PS00168; TRP_SYNTHASE_BETA; 1.
KW Tryptophan biosynthesis; Pyridoxal phosphate (BY SIMILARITY).
FT BINDING 86 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
SQ SEQUENCE 399 AA; 42427 MW; DEBFD45D2C859C30 CRC64;

Query Match 20.0%; Score 56.5; DB 1; Length 399;
Best Local Similarity 36.2%; Pred. No. 6.4;
Matches 17; Conservative 9; Mismatches 12; Indels 9; Gaps 2;

QY 14 IVLKNLYFHKNMYPSPKLSFQAEFLFFLLILKN-----PLILCS 54
DB 19 ILMPALYQLEKNFVDKDSNFQKS---FFNLYKNYAGRPPLILCN 62

RESULT 5
CKR7_MOUSE
ID CKR7_MOUSE STANDARD; PRT; 378 AA.
AC P47774;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE C-C chemokine receptor type 7 precursor (C-C CKR-7) (CCR-7)
DE (MIP-3 beta receptor) (EBV-induced G protein-coupled receptor 1)
DE (EBI1).
GN CKR7 OR CMKBR7 OR EBI1 OR EBI1H.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6 X CBA; TISSUE=Thymus;
RX MEDLINE=95154835; PubMed=7851893;
RA Schweickart V.L., Raport C.J., Godiska R., Byers M.G., Eddy R.L. Jr.,
RA Shows T.B., Gray P.W.;
RT "Cloning of human and mouse EBI1, a lymphoid-specific
RT G-protein-coupled receptor encoded on human chromosome 17q12-q21.2.";
RL Genomics 23:643-650(1994).
CC -!- FUNCTION: RECEPTOR FOR THE MIP-3-BETA CHEMOKINE. PROBABLE MEDIATOR
CC OF EBV EFFECTS ON B LYMPHOCYTES OR OF NORMAL LYMPHOCYTE FUNCTIONS.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC -----
DR EMBL; L31580; AAA74232.1; -.
DR MGD; MGI:103011; Cmkbr7.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR_FL_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECEPTOR_FL_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 378 C-C CHEMOKINE RECEPTOR TYPE 7.
FT DOMAIN 25 59 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 60 86 1 (POTENTIAL).
FT DOMAIN 87 95 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 96 116 2 (POTENTIAL).
FT DOMAIN 117 130 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 131 152 3 (POTENTIAL).

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Page 3

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4.

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Query Match          19.1%; Score 54; DB 1; Length 633;
Best Local Similarity 41.0%; Pred. No. 21;
Matches 16; Conservative 4; Mismatches 15; Indels 4; Gaps 2;

QY 17 KNLVFKHNSMT-PSPKLSSFOEAFLEFFFLIL---KNPLT 51
      || ||| : ||| : ||| : ||| : ||| : |||
DB 286 KKNYFDKNSQHIPDKRRKQNEPGMRLEFLVWDEKNIILT 324

RESULT 10
UL16_HCMVA
ID UL16_HCMVA STANDARD; PRT; 230 AA.
AC P16757;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last annotation update)
DE Hypothetical protein UL16.
GN UL16.
OS Human cytomegalovirus (strain AD169).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Betaherpesvirinae; Cytomegalovirus.
OX NCBI_TaxID=10360;
RN [1]
RZ
RP SEQUENCE FROM N.A.
RX MEDLINE=90269039; PubMed=2161319;
RA Chiee M.S., Bankier A.T., Beck S., Bohni R., Brown C.M., Cerny R.,
RA Horsnell T., Hutchison C.A. III, Kouzarides T., Martignetti J.A.,
RA Reddick E., Satchwell S.C., Tomlinson P., Weston K.M., Barrell B.G.;
RA "Analysis of the protein-coding content of the sequence of human
RA cytomegalovirus strain AD169.";
RL Curr. Top. Microbiol. Immunol. 154:125-169(1990).
RC
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CC -----
CC EMBL; X17403; CAA35448.1; -.
DR DR
DR PIR; S09778; S09778.
KW Hypothetical protein.
FT CARBOHYD 35 35 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 41 41 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 68 68 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 84 84 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 95 95 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 101 101 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 132 132 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 145 145 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 230 AA; 26147 MW; B72F2C241C569967 CRC64;

Query Match          18.7%; Score 53; DB 1; Length 230;
Best Local Similarity 23.8%; Pred. No. 11;
Matches 15; Conservative 8; Mismatches 16; Indels 24; Gaps 2;

QY 15 VLKNLFFKHNSMP-----SPKLSSFOE-----AFLFFFLILKNPL 50
      ::: ||| : ||| : ||| : ||| : |||
DB 150 IIERLYVRLGSLYPRPPGSLAKHPKSVSADDELSATLARDIVLVSAITLFFFLALRIQP 209

QY 51 TLC 53
DB 210 RLC 212

RESULT 11
AQP5_HUMAN
ID AQP5_HUMAN STANDARD; PRT; 265 AA.
AC P55064;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)

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DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Aquaporin 5.
OS Homo sapiens (Human).
GN AQP5.
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96224064; PubMed=8621489;
RA Lee M.D., Bhakta K.Y., Raina S., Yonescu R., Griffin C.A.,
RA Copeland N.G., Gilbert D.J., Jenkins N.A., Preston G.M., Agre P.;
RT "The human Aquaporin-5 gene. Molecular characterization and
RT chromosomal localization."
RL J. Biol. Chem. 271:8599-8604(1996).
CC -!- FUNCTION: FORMS A WATER-SPECIFIC CHANNEL. IMPLICATED IN THE
CC GENERATION OF SALIVA, TEARS, AND PULMONARY SECRETIONS.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO THE MIP/AQUAPORIN FAMILY (TC 1.A.8).
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CC -----
DR EMBL; U46569; AAC50474.1; -.
DR EMBL; U46567; AAC50474.1; JOINED.
DR EMBL; U46568; AAC50474.1; JOINED.
DR HSP; P29972; LH61.
DR Genew; HGNC:638; AQP5.
DR MIM; 600442; -.
DR InterPro; IPR000425; MIP_family.
DR Pfam; PF00230; MIP; 1.
DR PRINTS; PR00783; MINTRINSCP.
DR ProDom; PD000295; MIP_family; 1.
DR TIGRfams; TIGR00861; MIP; 1.
DR PROSITE; PS00221; MIP; 1.
DR TransPro; Transmembrane.
KW DOMAIN 1 12 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 13 33 POTENTIAL.
FT TRANSMEM 34 36 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 37 57 POTENTIAL.
FT TRANSMEM 58 87 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 88 108 POTENTIAL.
FT TRANSMEM 109 126 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 127 147 POTENTIAL.
FT TRANSMEM 148 161 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 162 182 POTENTIAL.
FT TRANSMEM 183 205 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 206 226 POTENTIAL.
FT TRANSMEM 227 265 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 124 124 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 125 125 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 265 AA; 28292 MW; 053C10E6A17EAFDA CRC64;

Query Match 18.7%; Score 53; DB 1; Length 265;
Best Local Similarity 27.1%; Pred. No. 12;
Matches 19; Conservative 8; Mismatches 17; Indels 26; Gaps 2;

QY 9 LGIGLIY----LKNLYPHKNSMYP-----PKLSSFQEAFLFF 42
| | | | | | | | | | | | | | | | | | | | | | | |
Db 163 LSIGLSYTLGLHVGIIYFTGCSMNPARGFAGVVMNRFSPAHWFVWGPVIGVLAALTYF 222
| | | | | | | | | | | | | | | | | | | | | | | |

QY 43 FLILKNPLTL 52
| | | | | | | | | | | | | | | | | | | | | | | |
Db 223 YLLFPNLSL 232
| | | | | | | | | | | | | | | | | | | | | | | |

RESULT 12
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OS Vaccinia virus (strain Copenhagen).
OC Viruses; GSDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10249;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91021027; PubMed=2219722;
RA Goebel S.J., Johnson G.P., Perkins M.E., Davis S.W., Winslow J.P.,
RA Paoletti E.;
RT "The complete DNA sequence of vaccinia virus.";
RL Virology 179:247-266(1990).
RN [2]
RP COMPLETE GENOME.
RA Goebel S.J., Johnson G.P., Perkins M.E., Davis S.W., Winslow J.P.,
RA Paoletti E.;
RT "Appendix to 'The complete DNA sequence of vaccinia virus'.";
RL Virology 179:517-563(1990).
CC -!- FUNCTION: PRECURSOR FOR ONE OF THE TWO MOST ABUNDANT STRUCTURAL
CC COMPONENT OF THE VIRION (MAJOR CORE PROTEINS 4A AND 4B).
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CC -----
DR EMBL; M35027; AAA48118.1; -.
DR PIR; E42517; FOVZ5R.
DR InterPro; IPR004972; Pox_P4B.
DR Pfam; PF03292; Pox_P4B; 1.
KW Core protein.
FT PROPEP 1 61 BY SIMILARITY.
FT CHAIN 62 644 MAJOR CORE PROTEIN P4B.
SQ SEQUENCE 644 AA; 72624 MW; 76CC2ED6781F88A2 CRC64;

Query Match 18.7%; Score 53; DB 1; Length 644;
Best Local Similarity 29.5%; Pred. No. 29;
Matches 13; Conservative 11; Mismatches 20; Indels 0; Gaps 0;

OY 8 VLIGLIVLKNLYPHKNSMYPKLSFQEAFLFFFLILKNPLT 51
Db 239 LFGIKLPALENAYVHGDTYSLIQQLYEPKVKSYNMLLVNRLT 282

Search completed: November 21, 2002, 13:41:50
Job time : 13 secs
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GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: November 21, 2002, 13:40:47 ; Search time 29 Seconds  
(without alignments)  
383.674 Million cell updates/sec

Title: US-09-776-724A-142

Perfect score: 283

Sequence: 1 MRRCVRHVLGIGLIVLNKLY.....FQEAFLFFLLIKNPLTLC 54

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 205047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_rvirus:\*
- 16: sp\_bacteriaph:\*
- 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	63	22.3	395	10 Q9STW2	Q9stw2 arabidopsis
2	60	21.2	221	17 Q26431	Q26431 methanobact
3	59	20.8	272	4 Q9NQ00	Q9nqn0 homo sapien
4	58.5	20.7	325	13 Q918C2	Q918c2 xenopus lae
5	58.5	20.7	612	10 Q24437	Q24437 oryza longi
6	58	20.5	401	10 Q82159	Q82159 populus nig
7	58	20.5	440	8 Q9BB39	Q9bb39 dichaea mur
8	58	20.5	446	8 Q9BBP4	Q95bp4 pascatorea
9	58	20.5	452	8 Q9BB32	Q9bb32 pascatorea
10	58	20.5	457	8 Q9BB33	Q9bb33 chondrorrhyn
11	58	20.5	486	8 Q9BB38	Q9bb38 dichaea neg
12	58	20.5	559	5 Q24788	Q24788 echinococcu
13	58	20.5	795	5 Q8SS65	Q8ss65 encaphalito
14	57.5	20.3	170	16 Q8ZHG6	Q8zhg6 yersinia pe
15	57	20.1	503	8 Q9BB34	Q9bb34 cryptarhen
16	56.5	20.0	69	1 Q9C4Y2	Q9c4y2 sulfolobus

17	56.5	20.0	678	5 Q94736	Q94736 stomoxys ca
18	56.5	20.0	844	13 Q93552	Q93552 carassius a
19	56	19.8	119	8 Q8WF21	Q8wf21 bhutanitis
20	56	19.8	177	12 Q9YVZ0	Q9yvz0 melanoplus
21	56	19.8	225	17 Q8THM5	Q8tht5 methanosarc
22	56	19.8	459	8 Q9BB37	Q9bb37 warrea warr
23	56	19.8	472	10 Q9LPL5	Q9lpl5 arabidopsis
24	56	19.8	472	10 Q9ZT57	Q9zt57 arabidopsis
25	56	19.8	491	16 Q8Y8L4	Q8y8l4 listeria mo
26	56	19.8	494	16 Q92DD2	Q92dd2 listeria in
27	56	19.8	604	2 Q9RMC9	Q9rmc9 acinetobact
28	56	19.8	706	17 Q9YAG6	Q9yag6 aeropyrum p
29	55.5	19.6	217	8 Q9B6Q1	Q9b6q1 eulachnus s
30	55.5	19.6	297	5 Q9XWR3	Q9xwr3 caenorhabdi
31	55.5	19.6	329	17 Q28580	Q28580 archaeoglob
32	55.5	19.6	345	4 Q96MA5	Q96ma5 homo sapien
33	55.5	19.6	385	16 Q8X9T6	Q8x9t6 escherichia
34	55.5	19.6	458	13 Q93555	Q93555 carassius a
35	55.5	19.6	1146	12 Q914N7	Q914n7 rice black
36	55.5	19.6	1146	12 Q8U209	Q8u209 rice black
37	55.5	19.6	2295	12 Q91TP1	Q91tp1 tupaiia herp
38	55	19.4	510	8 Q9BAZ7	Q9baz7 soterosanth
39	55	19.4	510	8 Q9BAZ5	Q9baz5 kegeliiella
40	55	19.4	510	8 Q9BAZ4	Q9baz4 kegeliiella
41	55	19.4	769	10 Q9LHM0	Q9lhm0 arabidopsis
42	54.5	19.3	379	10 Q94447	Q94447 arabidopsis
43	54.5	19.3	441	2 Q34007	Q34007 staphylococ
44	54.5	19.3	675	5 Q9N5I3	Q9n5i3 caenorhabdi
45	54.5	19.3	1757	11 Q70481	Q70481 mus musculu

## ALIGNMENTS

## RESULT 1

Q9STW2	PRELIMINARY;	PRT;	395 AA.
AC Q9STW2			
DT 01-MAY-2000	(TrEMBLrel. 13, Created)		
DT 01-MAY-2000	(TrEMBLrel. 13, Last sequence update)		
DE Hypothetical	45.7 kDa protein.		
GN T22A6.150 OR A74G24320.			
OS Arabidopsis thaliana	(Mouse-ear cross).		
OC Eukaryota; Viridiplantae;	Embryophyta; Tracheophyta;		
OC Spermatophyta; Magnoliophyta;	eudicotyledons; core eudicots; Rosidae;		
OC eurosids II; Brassicales; Brassicaceae;	Arabidopsis.		
OX NCBI_TaxID=3702;			
RN [1]			
RP SEQUENCE FROM N.A.			
RA Bevan M., Zimmermann W., Grueneisen A., Wambutt R., Bancroft I.,			
RA Mewes H.W., Mayer K.F.X., Lemcke K., Schueller C.;			
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.			
RN [2]			
RP SEQUENCE FROM N.A.			
RA EU Arabidopsis sequencing project;			
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.			
RN [3]			
RP SEQUENCE FROM N.A.			
RA Zimmermann W., Grueneisen A., Wambutt R., Kalicki J., Wohldmann P.,			
RA Smith A., Mewes H.W., Lemcke K., Mayer K.F.X.;			
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.			
RN [4]			
RP SEQUENCE FROM N.A.			
RA EU Arabidopsis sequencing project;			
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.			
DR EMBL; AL086637; CAB45067.1; -			
DR EMBL; AL161561; CAB79342.1; -			
DR InterPro; IPR002203; InterPro.			
DR PROSITE; PS00881; PROSITE_SPLICING; UNKNOWN_1.			
KW Hypothetical protein.			
SQ SEQUENCE 395 AA; 45690 MW; EA8CE0F16E1E806D CRC64;			

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DR EMBL; AL135904; CAB99212.1; -.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
FT NON_TER 1
SQ SEQUENCE 272 AA; 30452 MW; 4FF5CF18077574CD CRC64;

Query Match 20.8%; Score 59; DB 4; Length 272;
Best Local Similarity 30.4%; Pred. No. 9.2; Indels 6; Gaps 2;
Matches 17; Conservative 9; Mismatches 24;

QY 2 RCVRHVIGLIGLVKLNLYFHKNMYPSPKLSFQEAFLFFFLILKNPL---TLCS 54
DB 200 RTCFSLCVGLVGTAIMYVGRYGNPK---EQKKYLLLFHSLFNPMLNPLICS 252

RESULT 4
Q918C2 PRELIMINARY; PRT; 325 AA.
AC Q918C2;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE Olfactory receptor class I.
DE Olfactory receptor class I.
GN XB242.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;
OC Xenopodinae; Xenopus.
OC NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=OLFACTORY EPITHELIUM;
RA Mezler M., Breer H.;
RT "Two classes of olfactory receptors: molecular and functional
RT studies.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ250752; CAC00723.1; -.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 325 AA; 37075 MW; 94CDE3DC322C97A4 CRC64;

Query Match 20.7%; Score 58.5; DB 13; Length 325;
Best Local Similarity 28.3%; Pred. No. 13; Indels 3; Gaps 1;
Matches 15; Conservative 7; Mismatches 28;

QY 4 CVRHVIGLIGLVKLNLYFHKNMYP---SPKLSFQEAFLFFFLILKNPLTLC 53
DB 244 CTHLLVIGLVFIPRLFVYSTSQIPLIPDLNVLICLYTFPHLSPFIIFC 296

RESULT 5
Q24437 PRELIMINARY; PRT; 612 AA.
AC Q24437;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Receptor kinase-like protein.
DE Oryza longistaminata (Long-staminate rice).
OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OC NCBI_TaxID=4528;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IRBB21;
RA Lovell J.;
RX MEDLINE=96106403; PubMed=8525370;
```

RA Song W.Y., Wang G.L., Chen L.L., Kim H.S., Pi L.Y., Holsten T.,  
 RA Gardner J., Wang B., Zhai W.X., Zhu L.H., Fauquet C., Ronald P.,  
 RT "A receptor kinase-like protein encoded by the rice disease resistance  
 RL gene, Xa21";  
 RN Science 270:1804-1806(1995).  
 RP [2]  
 RC SEQUENCE FROM N.A.  
 RX STRAIN=IRBB21;  
 RA Song W.Y., Pi L.Y., Wang G.L., Gardner J., Holsten T., Ronald P.C.;  
 RT "Evolution of the rice Xa21 disease resistance gene family";  
 RL Plant Cell 9:1279-1287(1997).  
 DR EMBL; U72726; AAB82753.1; -;  
 DR InterPro: IPR001611; LRR.  
 DR InterPro: IPR003592; LRR\_out.  
 DR Pfam: PF00560; LRR; 21.  
 DR PRINTS: PR00019; LEURICHRPT.  
 DR SMART: SM00370; LRR; 17.  
 KW Kinase.  
 SQ SEQUENCE 612 AA; 66380 MW; 9BE54BBB4242A91F CRC64;  
 Query Match 20.7%; Score 58.5; DB 10; Length 612;  
 Best Local Similarity 38.3%; Pred. No. 23;  
 Matches 18; Conservative 5; Mismatches 19; Indels 5; Gaps 2;  
 QY 1 MRCVRHVIGLIVLKNLYFHKNM---YFSP--KLSSFOEAFLEFF 42  
 Db 163 LRGMIPREIGASLKLNSLYLHKNLSGEISALGNLTSLQFDFLSF 209  
 RESULT 6  
 ID 082159 PRELIMINARY; PRT; 401 AA.  
 AC 082159;  
 DT 01-NOV-1998 (Tremblrel. 08, Created)  
 DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)  
 DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)  
 DE Phosphoglycerate kinase (EC 2.7.2.3).  
 GN PNCYTPGK2.  
 OS Populus nigra (Lombardy poplar).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids I; Malpighiales; Salicaceae; Populus.  
 OX NCBI\_TaxID=3691;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Nishiguchi M.;  
 RT "A cDNA clone encoding cytosolic phosphoglycerate kinase 2 from  
 RL Lombardy poplar";  
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.  
 CC -!- CATALYTIC ACTIVITY: ATP + 3-PHOSPHO-D-GLYCERATE = ADP + 3-  
 CC PHOSPHO-D-GLYCEROL PHOSPHATE.  
 CC -!- SUBUNIT: MONOMER (BY SIMILARITY).  
 CC -!- SIMILARITY: BELONGS TO THE PHOSPHOGLYCERATE KINASE FAMILY.  
 DR EMBL; AB018411; BAA33802.1; -;  
 DR HSSP; P18912; IHPH.  
 DR InterPro: IPR001576; PGK.  
 DR Pfam: PF00162; PGK; 1.  
 DR PRINTS: PR00477; PGLYCKINASE.  
 DR PROSITE; PS00111; PGLYCERATE\_KINASE; 1.  
 KW Glycolysis; Kinase; Transferase.  
 SQ SEQUENCE 401 AA; 42669 MW; 79B095EE6B1A9DA1 CRC64;  
 Query Match 20.5%; Score 58; DB 10; Length 401;  
 Best Local Similarity 29.5%; Pred. No. 18;  
 Matches 13; Conservative 11; Mismatches 16; Indels 4; Gaps 1;  
 QY 1 MRCVRHVIGLIVLKNLYFHKNMYPSP---KLSSFOEAFLE 40  
 Db 103 VEKLVAEIPGGVLLNFRFHEEKNDEFAKLAIAEIVV 146  
 RESULT 7  
 ID 09BB39 PRELIMINARY; PRT; 440 AA.  
 AC 09BB39;  
 DT 01-JUN-2001 (Tremblrel. 17, Created)  
 DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)  
 DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)  
 DE Probable intron maturase (Maturase K) (Fragment).  
 GN MATK.  
 OS Dichaena muricata.  
 OC Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Orchidaceae;  
 OC Epidendroideae; higher Epidendroideae; Maxillarieae; Zygopetalinae;  
 OC Dichaena.  
 OX NCBI\_TaxID=125110;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Whitten M., Williams N.H., Chase M.W.;  
 RT "Tribal and subtribal relationships of Maxillarieae (Orchidaceae) with  
 RL special emphasis on Stanhopeinae: Combined molecular evidence.";  
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases  
 CC -!- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II  
 CC INTRONS (BY SIMILARITY).  
 CC -!- SIMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS,  
 CC AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED BY  
 CC MITOCHONDRIAL INTRONS.  
 DR EMBL; AF239415; AAK31812.1; -;  
 DR InterPro: IPR000442; Intron\_maturase2.  
 DR InterPro: IPR002866; MatK\_N.  
 DR InterPro: IPR002016; Peroxidase.  
 DR Pfam: PF01346; Intron\_maturase2; 1.  
 DR Pfam: PF01824; MatK\_N; 1.  
 DR PROSITE; PS00436; PEROXIDASE\_2; UNKNOWN\_1.  
 KW Chloroplast; mRNA processing.  
 FT NON\_TER 1  
 FT NON\_TER 440 440  
 SQ SEQUENCE 440 AA; 52685 MW; CFFBAF87755FF9E5 CRC64;  
 Query Match 20.5%; Score 58; DB 8; Length 440;  
 Best Local Similarity 29.6%; Pred. No. 20;  
 Matches 16; Conservative 11; Mismatches 13; Indels 14; Gaps 2;  
 QY 13 LIVLKNLYFHKNMYPSP-----PKLSSFOEAFLEFFLLKKNPLTL 52  
 Db 262 LILMKKWKHLVNFQSTFWFQFYRIHIKLPNYSFSLGYFSIVLKNPLVV 315  
 RESULT 8  
 ID 095BP4 PRELIMINARY; PRT; 446 AA.  
 AC 095BP4;  
 DT 01-DEC-2001 (Tremblrel. 19, Created)  
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)  
 DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)  
 DE Probable intron maturase (Maturase K) (Fragment).  
 GN MATK.  
 OS Pescatorea lehmannii.  
 OC Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Orchidaceae;  
 OC Epidendroideae; higher Epidendroideae; Maxillarieae; Zygopetalinae;  
 OC Pescatorea.  
 OX NCBI\_TaxID=125160;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Williams N.H., Chase M.W., Fulcher T., Whitten M.W.;  
 RT "Molecular systematics of the Oncidiinae based on evidence from four  
 RT DNA sequence regions: expanded circumscriptions of Cyrtanthium,  
 RT Erycina, Otaglossum, and Trichocentrum, and a new genus  
 RT (Orchidaceae)";  
 RL Lindleyana 16:113-139(2001).  
 CC -!- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II  
 CC INTRONS (BY SIMILARITY).

AC	Q9BB33:
DT	01-JUN-2001 (TReMBLrel. 17, Created)
DT	01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DE	01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE	Probable intron maturase (Maturase K) (Fragment).
GN	MATK.
OS	Chondrorhyncha reichenbachiana.
OG	Chloroplast.
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC	Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Orchidaceae;
OC	Epidendroideae; higher Epidendroideae; Maxillariaceae; Zygopetalinae;
OC	Chondrorhyncha.
OX	NCBI_TaxID=125095;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	Whitten M., Williams N.H., Chase M.W.;
RT	"tribal and subtribal relationships of Maxillariaceae (Orchidaceae) with
RT	special emphasis on Stanhopeinae: Combined molecular evidence.";
RL	Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
CC	-I- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II
CC	INTRONS (BY SIMILARITY).
CC	-I- SIMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS,
CC	AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED BY
CC	MITOCHONDRIAL INTRONS.
DR	EMBL; AF239421; AAK31818.1; -.
DR	InterPro; IPR000005; HTHArac.
DR	InterPro; IPR000442; Intron_maturase2.
DR	InterPro; IPR002866; Matk.N.
DR	Pfam; PF01348; Intron_maturas2; 1.
DR	Pfam; PF01824; Matk.N.; 1.
DR	PROSITE; PS00041; HTH_ARAC_FAMILY_1; UNKNOWN_1.
KW	Chloroplast; mRNA processing.
FT	NON_TER 1
FT	NON_TER 457 457
FT	SEQUENCE 457 AA; 54601 MW; 06B18D9267078E9F CRC64;
QY	Query Match 20.5%; Score 58; DB 8; Length 457;
QY	Best Local Similarity 29.6%; Pred. NO. 20;
QY	Matches 16; Conservative 11; Mismatches 13; Indels 14; Gaps
DB	13 LIVLNLYFHKNMSPS-----PKLSFOEAFI-FFFLIKNPITL 52    ::   ::    ::  ::   ::
DB	273 LILMKKKHFLVFWGYSFHFWFQPYRTHIKLPNSPFLGYSVILKNPLVV 326    ::   ::    ::  ::   ::
RESULT 11	
Q9BB38	PRELIMINARY; PRT: 486 AA.
ID	Q9BB38:
AC	Q9BB38:
DT	01-JUN-2001 (TReMBLrel. 17, Created)
DT	01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT	01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE	Probable intron maturase (Maturase K) (Fragment).
GN	MATK.
OS	Dichaea neglecta.
OG	Chloroplast
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC	Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Orchidaceae;
OC	Epidendroideae; higher Epidendroideae; Maxillariaceae; Zygopetalinae;
OC	Dichaea.
OX	NCBI_TaxID=125111;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	Whitten M., Williams N.H., Chase M.W.;
RT	"tribal and subtribal relationships of Maxillariaceae (Orchidaceae) with
RT	special emphasis on Stanhopeinae: Combined molecular evidence.";
RL	Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
CC	-I- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II
CC	INTRONS (BY SIMILARITY).
CC	-I- SIMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS,
CC	AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED BY
CC	MITOCHONDRIAL INTRONS.
DR	EMBL; AF239416; AAK31813.1; -.

[illegible]



Result	Query No.	Score	% Match	Length	DB	ID	Description
1	283	100.0	54	1	PCT-US98-14613-142	Sequence 142, App	
2	283	100.0	54	16	US-09-229-982-142	Sequence 142, App	
3	283	100.0	54	20	US-09-669-688-142	Sequence 142, App	
4	283	100.0	54	21	US-09-776-724A-142	Sequence 142, App	
5	73	25.8	85	1	PCT-US01-01334-6555	Sequence 6555, Ap	
6	73	25.8	85	21	US-09-704-874-6555	Sequence 6555, Ap	

## ALIGNMENTS

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RESULT 1
PCT-US98-14613-142
; Sequence 142, Application PC/TUS9814613
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: 64 Human Secreted Proteins
; FILE REFERENCE: P201PCT
; CURRENT APPLICATION NUMBER: PCT/US98/14613
; CURRENT FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/052,870
; EARLIER FILING DATE: 1997-07-16
; NUMBER OF SEQ ID NOS: 178
; SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 142
LENGTH: 54
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US98-14613-142

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Query Match      100.0%; Score 283; DB 1; Length 54;
Best Local Similarity 100.0%; Pred. No. 1.4e-27;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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yy 1 MRRCVRHVIGLIVLKNYFHKNWSPKLSFQFAFLFFILKNPTLTCS 54  
|||||  
bb 1 MRRCVRHVIGLIVLKNYFHKNWSPKLSFQFAFLFFILKNPTLTCS 54  
|||||

us-09-776-724a-142.rapm

Thu Nov 21 16:07:40 2002

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US-09-229-982-142
; Sequence 142, Application US/09229982
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 64 Human Secreted Proteins
; FILE REFERENCE: PZ011P1
; CURRENT APPLICATION NUMBER: US/09/229,982
; CURRENT FILING DATE: 1999-01-14
; EARLIER APPLICATION NUMBER: 1998-07-15
; EARLIER FILING DATE: PCT/US98/14613
; EARLIER APPLICATION NUMBER: 1997-07-16
; EARLIER FILING DATE: 60/052,661
; EARLIER APPLICATION NUMBER: 1997-07-16
; EARLIER FILING DATE: 60/052,872
; EARLIER APPLICATION NUMBER: 1997-07-16
; EARLIER FILING DATE: 60/052,871
; EARLIER APPLICATION NUMBER: 1997-07-16
; EARLIER FILING DATE: 60/052,874
; EARLIER APPLICATION NUMBER: 1997-07-16
; EARLIER FILING DATE: 60/052,873
; EARLIER APPLICATION NUMBER: 1997-07-16
; EARLIER FILING DATE: 60/052,870
; EARLIER APPLICATION NUMBER: 1997-07-16
; EARLIER FILING DATE: 60/052,875
; EARLIER APPLICATION NUMBER: 1997-07-16
; EARLIER FILING DATE: 60/053,440
; EARLIER APPLICATION NUMBER: 1997-07-22
; EARLIER FILING DATE: 60/053,441
; EARLIER APPLICATION NUMBER: 1997-07-22
; EARLIER FILING DATE: 60/053,442
; EARLIER APPLICATION NUMBER: 1997-08-18
; EARLIER FILING DATE: 60/056,359
; EARLIER APPLICATION NUMBER: 1997-08-18
; EARLIER FILING DATE: 60/055,985
; EARLIER APPLICATION NUMBER: 1997-08-18
; EARLIER FILING DATE: 60/055,952
; EARLIER APPLICATION NUMBER: 1997-08-18
; EARLIER FILING DATE: 60/055,989
; EARLIER APPLICATION NUMBER: 1997-08-18
; EARLIER FILING DATE: 60/055,946
; EARLIER APPLICATION NUMBER: 1997-08-18
; EARLIER FILING DATE: 60/055,726
; EARLIER APPLICATION NUMBER: 1997-08-18
; EARLIER FILING DATE: 60/055,724
; EARLIER APPLICATION NUMBER: 1997-08-18
; EARLIER FILING DATE: 60/055,946
; EARLIER APPLICATION NUMBER: 1997-08-18
; EARLIER FILING DATE: 60/055,683
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 142
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-229-982-142

Query Match      100.0%; Score 283; DB 16; Length 54;
Best Local Similarity 100.0%; Pred. No. 1.4e-27;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRRCVRHVLGIGLIVLKNLYFHKNMYPSPKLSFQEAFLFFLLILKNPLTICS 54
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Db 1 MRRCVRHVLGIGLIVLKNLYFHKNMYPSPKLSFQEAFLFFLLILKNPLTICS 54

RESULT 3
US-09-669-688-142
; Sequence 142, Application US/09669688
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 64 Human Secreted Proteins

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; FILE REFERENCE: PZ011P1
; CURRENT APPLICATION NUMBER: US/09/669,688
; CURRENT FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/09/229,982
; PRIOR FILING DATE: 1999-01-14
; PRIOR APPLICATION NUMBER: PCT/US98/14613
; PRIOR FILING DATE: 1998-07-15
; PRIOR APPLICATION NUMBER: 60/052,661
; PRIOR FILING DATE: 1997-07-16
; PRIOR APPLICATION NUMBER: 60/052,872
; PRIOR FILING DATE: 1997-07-16
; PRIOR APPLICATION NUMBER: 60/052,871
; PRIOR FILING DATE: 1997-07-16
; PRIOR APPLICATION NUMBER: 60/052,874
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; PRIOR APPLICATION NUMBER: 60/052,870
; PRIOR FILING DATE: 1997-07-16
; PRIOR APPLICATION NUMBER: 60/052,875
; PRIOR FILING DATE: 1997-07-22
; PRIOR APPLICATION NUMBER: 60/053,440
; PRIOR FILING DATE: 1997-07-22
; PRIOR APPLICATION NUMBER: 60/053,441
; PRIOR FILING DATE: 1997-07-22
; PRIOR APPLICATION NUMBER: 60/053,442
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/056,359
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,725
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,985
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,952
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,989
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/056,361
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,726
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,724
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,946
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,683
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 142
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-669-688-142

Query Match      100.0%; Score 283; DB 20; Length 54;
Best Local Similarity 100.0%; Pred. No. 1.4e-27;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRRCVRHVLGIGLIVLKNLYFHKNMYPSPKLSFQEAFLFFLLILKNPLTICS 54
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Db 1 MRRCVRHVLGIGLIVLKNLYFHKNMYPSPKLSFQEAFLFFLLILKNPLTICS 54

RESULT 4
US-09-776-724a-142
; Sequence 142, Application US/09776724A
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 64 Human Secreted Proteins
; FILE REFERENCE: PZ011
; CURRENT APPLICATION NUMBER: US/09/776,724A
; CURRENT FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/180,909

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; PRIOR FILING DATE: 2000-02-08
; PRIOR APPLICATION NUMBER: 09/659,688
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: 09/229,982
; PRIOR FILING DATE: 1999-01-14
; PRIOR APPLICATION NUMBER: PCT/US98/14613
; PRIOR FILING DATE: 1998-07-15
; PRIOR APPLICATION NUMBER: 60/052,661
; PRIOR FILING DATE: 1997-07-16
; PRIOR APPLICATION NUMBER: 60/052,872
; PRIOR FILING DATE: 1997-07-16
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; PRIOR FILING DATE: 1997-07-16
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; PRIOR APPLICATION NUMBER: 60/052,870
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; PRIOR APPLICATION NUMBER: 60/053,440
; PRIOR FILING DATE: 1997-07-22
; PRIOR APPLICATION NUMBER: 60/053,441
; PRIOR FILING DATE: 1997-07-22
; PRIOR APPLICATION NUMBER: 60/053,442
; PRIOR FILING DATE: 1997-07-22
; PRIOR APPLICATION NUMBER: 60/056,359
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,725
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; PRIOR FILING DATE: 1997-08-18
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; PRIOR FILING DATE: 1997-08-18
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; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/056,361
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,726
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,724
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,946
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,683
; PRIOR FILING DATE: 1997-08-18
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 142
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-776-724A-142

Query Match 100.0%; Score 283; DB 21; Length 54;
Best Local Similarity 100.0%; Pred. No. 1.4e-27;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRRCVHVLGIGLVKKNLYFHKNMSPKLSFQEAFLFFLLKKNPLTICS 54
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Db 1 MRRCVHVLGIGLVKKNLYFHKNMSPKLSFQEAFLFFLLKKNPLTICS 54
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RESULT 5
PCT-US01-01334-6555
; Sequence 6555, Application PC/TUS0101334
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc., et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC010PCT
; CURRENT APPLICATION NUMBER: PCT/US01/01334
; CURRENT FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/214,886
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/217,487
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,758
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,963
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/217,496
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; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/225,267
; PRIOR FILING DATE: 2000-08-14
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; PRIOR FILING DATE: 2000-07-07
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; PRIOR APPLICATION NUMBER: 60/220,964
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/241,809
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/249,299
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/236,327
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/241,785
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/244,617
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 60/225,268
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/236,368
; PRIOR FILING DATE: 2000-09-29
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; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/251,868
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/229,344
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/234,997
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: 60/229,343
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/229,345
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PRIOR APPLICATION NUMBER: 60/249,211	
PRIOR FILING DATE: 2000-11-17	
PRIOR APPLICATION NUMBER: 60/249,215	
PRIOR FILING DATE: 2000-11-17	
PRIOR APPLICATION NUMBER: 60/249,216	
PRIOR FILING DATE: 2000-11-17	
PRIOR APPLICATION NUMBER: 60/249,264	
PRIOR FILING DATE: 2000-11-17	
PRIOR APPLICATION NUMBER: 60/249,214	
PRIOR FILING DATE: 2000-11-17	
PRIOR APPLICATION NUMBER: 60/249,297	
PRIOR FILING DATE: 2000-11-17	
PRIOR APPLICATION NUMBER: 60/232,400	
PRIOR FILING DATE: 2000-09-14	
PRIOR APPLICATION NUMBER: 60/231,232	
PRIOR FILING DATE: 2000-09-08	
PRIOR APPLICATION NUMBER: 60/232,081	
PRIOR FILING DATE: 2000-09-08	
PRIOR APPLICATION NUMBER: 60/232,080	
PRIOR FILING DATE: 2000-09-08	
PRIOR APPLICATION NUMBER: 60/231,414	
PRIOR FILING DATE: 2000-09-08	
PRIOR APPLICATION NUMBER: 60/231,244	
PRIOR FILING DATE: 2000-09-08	
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PRIOR FILING DATE: 2000-09-14	
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PRIOR FILING DATE: 2000-09-14	
PRIOR APPLICATION NUMBER: 60/232,401	
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PRIOR FILING DATE: 2000-10-20	
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PRIOR APPLICATION NUMBER: 60/241,221	
PRIOR FILING DATE: 2000-10-20	
PRIOR APPLICATION NUMBER: 60/246,475	
PRIOR FILING DATE: 2000-11-08	
PRIOR APPLICATION NUMBER: 60/231,243	
PRIOR FILING DATE: 2000-09-08	
PRIOR APPLICATION NUMBER: 60/233,065	
PRIOR FILING DATE: 2000-09-14	
PRIOR APPLICATION NUMBER: 60/232,398	

[illegible]

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US-09-764-874-6555
; Sequence 6555, Application US/09764874
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC010
; CURRENT APPLICATION NUMBER: US/09/764,874
; CURRENT FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/214,886
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/217,487

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;	PRIOR APPLICATION NUMBER: 60/2239, 503
;	PRIOR FILING DATE: 2000-09-05
;	PRIOR APPLICATION NUMBER: 60/236, 367
;	PRIOR FILING DATE: 2000-09-29
;	PRIOR APPLICATION NUMBER: 60/237, 039
;	PRIOR FILING DATE: 2000-10-02
;	PRIOR APPLICATION NUMBER: 60/237, 038
;	PRIOR FILING DATE: 2000-10-02
;	PRIOR APPLICATION NUMBER: 60/236, 370
;	PRIOR FILING DATE: 2000-09-29
;	PRIOR APPLICATION NUMBER: 60/236, 802
;	PRIOR FILING DATE: 2000-10-02
;	PRIOR APPLICATION NUMBER: 60/237, 037
;	PRIOR FILING DATE: 2000-10-02
;	PRIOR APPLICATION NUMBER: 60/237, 040
;	PRIOR FILING DATE: 2000-10-02
;	PRIOR APPLICATION NUMBER: 60/240, 960
;	PRIOR FILING DATE: 2000-10-20
;	PRIOR APPLICATION NUMBER: 60/239, 935
;	PRIOR FILING DATE: 2000-10-13
;	PRIOR APPLICATION NUMBER: 60/239, 937
;	PRIOR FILING DATE: 2000-10-13
;	PRIOR APPLICATION NUMBER: 60/241, 787
;	PRIOR FILING DATE: 2000-10-20
;	PRIOR APPLICATION NUMBER: 60/246, 474
;	PRIOR FILING DATE: 2000-11-08
;	PRIOR APPLICATION NUMBER: 60/246, 532
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;	PRIOR APPLICATION NUMBER: 60/249, 216
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;	PRIOR APPLICATION NUMBER: 60/249, 210
;	PRIOR FILING DATE: 2000-11-17
;	PRIOR APPLICATION NUMBER: 60/226, 681
;	PRIOR FILING DATE: 2000-08-22
;	PRIOR APPLICATION NUMBER: 60/225, 759
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;	PRIOR APPLICATION NUMBER: 60/225, 214
;	PRIOR FILING DATE: 2000-08-14
;	PRIOR APPLICATION NUMBER: 60/235, 836
;	PRIOR FILING DATE: 2000-09-27
;	PRIOR APPLICATION NUMBER: 60/230, 438
;	PRIOR FILING DATE: 2000-09-06
;	PRIOR APPLICATION NUMBER: 60/215, 135
;	PRIOR FILING DATE: 2000-06-30
;	PRIOR APPLICATION NUMBER: 60/225, 266
;	PRIOR FILING DATE: 2000-08-14
;	PRIOR APPLICATION NUMBER: 60/249, 218
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;	PRIOR FILING DATE: 2000-11-17
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;	PRIOR FILING DATE: 2000-11-17
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;	PRIOR FILING DATE: 2000-11-17
;	PRIOR APPLICATION NUMBER: 60/249, 211
;	PRIOR FILING DATE: 2000-11-17
;	PRIOR APPLICATION NUMBER: 60/249, 215
;	PRIOR FILING DATE: 2000-11-17
;	PRIOR APPLICATION NUMBER: 60/249, 264
;	PRIOR FILING DATE: 2000-11-17
;	PRIOR APPLICATION NUMBER: 60/249, 214

Query Match 25.8%; Score 73; DB 21; Length 85;  
Best Local Similarity 30.5%; Pred. No. 0.67;  
Matches 18; Conservative 11; Mismatches 16; Indels 14; Gaps 2;  
QY 1 MRRC-----VRLVGLIGLIVLKNLYFHKNSMYPSPKLSFQEAFLFFFLIKNPLTLC 53  
DB 6 LRECLLMTCTIRTAGRMHILKSLQF-----GQKNPQEQFAVFLVVKVPILFC 56

RESULT 7  
US-09-809-391-362  
; Sequence 362, Application US/09809391  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: 186 Human Secreted proteins  
; FILE REFERENCE: P2002P2  
; CURRENT APPLICATION NUMBER: US/09/809,391  
; CURRENT FILING DATE: 2001-03-16  
; Prior application data removed - consult PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 761  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 362  
; LENGTH: 132  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (132)  
; OTHER INFORMATION: xaa equals stop translation  
US-09-809-391-362

Query Match 22.8%; Score 64.5; DB 22; Length 132;

Best Local Similarity 30.5%; Pred. No. 0.67;  
Matches 18; Conservative 11; Mismatches 16; Indels 14; Gaps 2;

QY 1 MRRC-----VRLVGLIGLIVLKNLYFHKNSMYPSPKLSFQEAFLFFFLIKNPLTLC 53  
DB 6 LRECLLMTCTIRTAGRMHILKSLQF-----GQKNPQEQFAVFLVVKVPILFC 56

RESULT 7  
US-09-809-391-362  
; Sequence 362, Application US/09809391  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: 186 Human Secreted proteins  
; FILE REFERENCE: P2002P2  
; CURRENT APPLICATION NUMBER: US/09/809,391  
; CURRENT FILING DATE: 2001-03-16  
; Prior application data removed - consult PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 761  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 362  
; LENGTH: 132  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (132)  
; OTHER INFORMATION: xaa equals stop translation  
US-09-809-391-362

Best Local Similarity 37.5%; Pred. No. 12;  
Matches 21; Conservative 9; Mismatches 9; Indels 17; Gaps 5;  
QY 1 MRRCVRH-VLIGLIGLIVLKNLYFHKNSMYPSPKLSFQEAFLFFFLIL 46  
DB 1 MECHLYHSVHGI-----NPYIHKNT-HPSINIMVWDEQVNSFEREFVFFFLII 49

RESULT 8  
US-09-882-171-362  
; Sequence 362, Application US/09882171  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: 186 Human Secreted proteins  
; FILE REFERENCE: P2002P2  
; CURRENT APPLICATION NUMBER: US/09/882,171  
; CURRENT FILING DATE: 2001-06-18  
; Prior application data removed - consult PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 761  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 362  
; LENGTH: 132  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (132)  
; OTHER INFORMATION: xaa equals stop translation  
US-09-882-171-362

; PRIOR APPLICATION NUMBER: 60/047,596  
 ; PRIOR FILING DATE: 1997-05-23  
 ; PRIOR APPLICATION NUMBER: 60/047,612  
 ; PRIOR FILING DATE: 1997-05-23  
 ; PRIOR APPLICATION NUMBER: 60/047,632  
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 ; PRIOR APPLICATION NUMBER: 60/047,601  
 ; PRIOR FILING DATE: 1997-05-23  
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 ; PRIOR FILING DATE: 1997-04-11  
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 ; PRIOR APPLICATION NUMBER: 60/043,669  
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 ; PRIOR APPLICATION NUMBER: 60/048,974  
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 ; PRIOR APPLICATION NUMBER: 60/056,864

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 ; PRIOR APPLICATION NUMBER: 60/057,669  
 ; PRIOR FILING DATE: 1997-09-05  
 ; PRIOR APPLICATION NUMBER: 60/049,610

Query Match 22.8%; Score 64.5; DB 22; Length 132;  
 Best Local Similarity 37.5%; Pred. No. 12;  
 Matches 21; Conservative 9; Mismatches 9; Indels 17; Gaps 5;

QY 1 MRCVRH-VLGLIVLKNLYFKHKNMYP-----PKLSSQFAFL-FFFLIL 46  
 DB 1 MBHCLYHSVHGI-----NPYTHKNT-HPSINIYMWDEQVNSFERFVPPFFLII 49

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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 218
; LENGTH: 89
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-01330-218

Query Match      22.6%; Score 64; DB 1; Length 89;
Best Local Similarity 60.0%; Pred. No. 9.6;
Matches 12; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 13 LIVLKNLYFHKNMYPSPKL 32
      |||||: :| :|: |||:|
Db 13 LIVLKSFFFFKDSLTPSPRL 32

RESULT 12
PCT-US01-01339-4675
; Sequence 4675, Application PC/TUS0101339
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc., et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006PCT
; CURRENT APPLICATION NUMBER: PCT/US01/01339
; CURRENT FILING DATE: 2001-03-17
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4675
; LENGTH: 89
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-01339-4675

Query Match      22.6%; Score 64; DB 1; Length 89;
Best Local Similarity 60.0%; Pred. No. 9.6;
Matches 12; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 13 LIVLKNLYFHKNMYPSPKL 32
      |||||: :| :|: |||:|
Db 13 LIVLKSFFFFKDSLTPSPRL 32

RESULT 13
PCT-US01-01339-5353
; Sequence 5353, Application PC/TUS0101339
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc., et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006PCT
; CURRENT APPLICATION NUMBER: PCT/US01/01339
; CURRENT FILING DATE: 2001-03-17
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5353
; LENGTH: 89
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-01339-5353

Query Match      22.6%; Score 64; DB 1; Length 89;
Best Local Similarity 60.0%; Pred. No. 9.6;
Matches 12; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 13 LIVLKNLYFHKNMYPSPKL 32
      |||||: :| :|: |||:|
Db 13 LIVLKSFFFFKDSLTPSPRL 32

RESULT 14
US-09-764-891-4675
; Sequence 4675, Application US/09764891
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.

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; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4675
; LENGTH: 89
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-891-4675
```

```
Query Match      22.6%; Score 64; DB 21; Length 89;
Best Local Similarity 60.0%; Pred. NO. 9.6;
Matches 12; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
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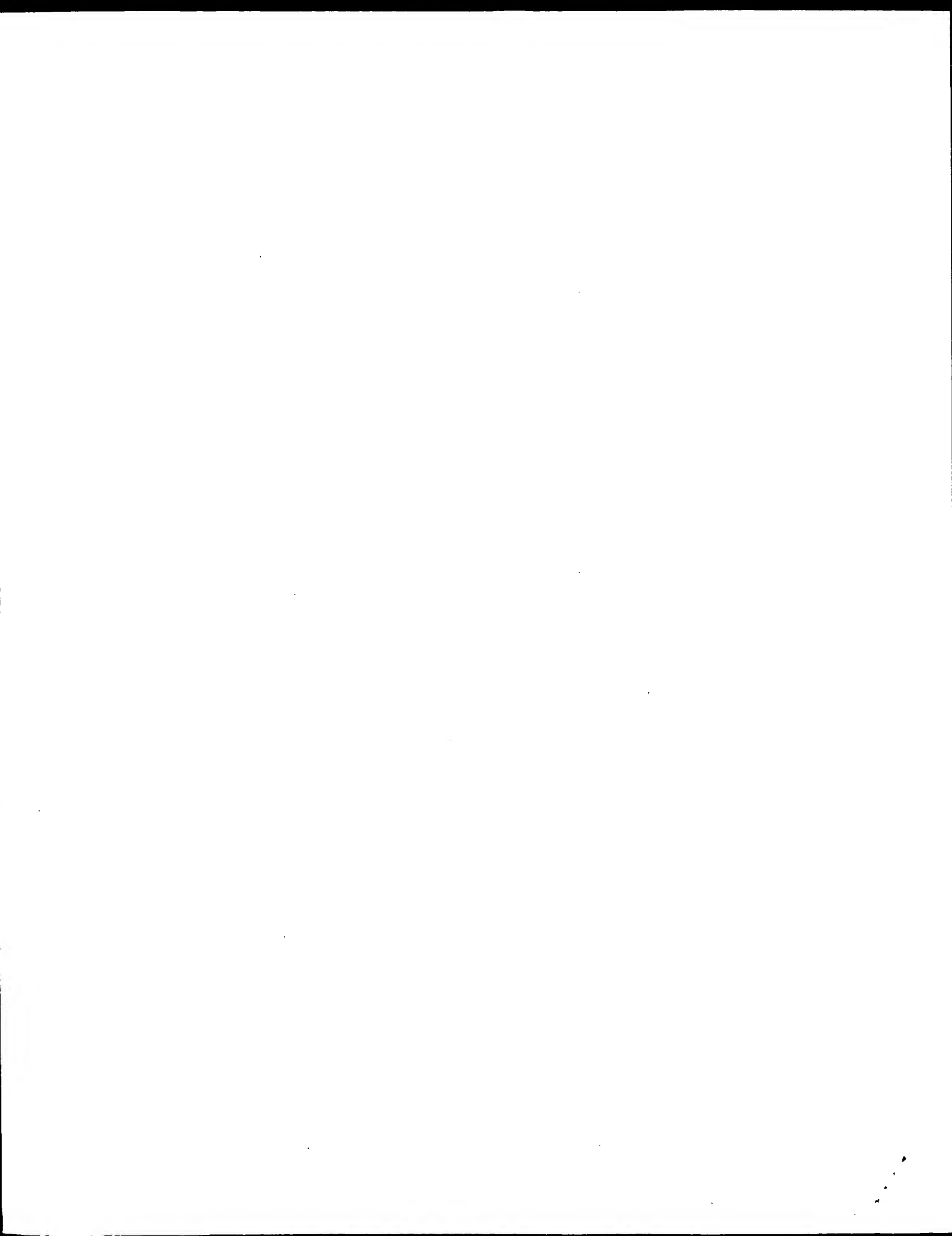
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QY 13 LIVLKNLYFHKNMYPSPKL 32
      ||||: :| |:| :|||:|
Db 13 LIVLKSFFFFFKDSLTPSPRL 32
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RESULT 15
US-09-764-891-5353
; Sequence 5353, Application US/09764891
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5353
; LENGTH: 89
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-891-5353
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```
Query Match      22.6%; Score 64; DB 21; Length 89;
Best Local Similarity 60.0%; Pred. NO. 9.6;
Matches 12; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
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```
QY 13 LIVLKNLYFHKNMYPSPKL 32
      ||||: :| |:| :|||:|
Db 13 LIVLKSFFFFFKDSLTPSPRL 32
```

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Job time : 143 secs
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GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 21, 2002, 13:41:56 ; Search time 10 seconds  
(without alignments)  
186.011 Million cell updates/sec

Title: US-09-776-724A-142

Perfect score: 283

Sequence: 1 MRRCVRHVLGILVILKNLY.....FQEAFLFFLLKKNPLTICS 54

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 99223 seqs, 3446456 residues

Total number of hits satisfying chosen parameters: 99223

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

#### Database :

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2: /cgn2\_6/ptodata1/paa/US06\_NEW\_COMB.pep.\*  
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4: /cgn2\_6/ptodata1/paa/US08\_NEW\_COMB.pep.\*  
5: /cgn2\_6/ptodata1/paa/US09\_NEW\_COMB.pep.\*  
6: /cgn2\_6/ptodata1/paa/US10\_NEW\_COMB.pep.\*  
7: /cgn2\_6/ptodata1/paa/US60\_NEW\_COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	58.5	20.7	673	6	US-10-092-411A-4480
2	55.5	19.6	172	6	US-10-264-237-1435
3	52.5	18.6	655	5	US-09-724-676-69043
4	52	18.4	716	6	US-10-230-437-190
5	52	18.4	716	6	US-10-131-813A-512
6	52	18.4	716	6	US-10-131-819A-512
7	52	18.4	716	6	US-10-131-823A-512
8	52	18.4	716	6	US-10-131-826A-512
9	52	18.4	716	6	US-10-131-829A-512
10	52	18.4	716	6	US-10-131-829A-512
11	52	18.4	716	6	US-10-125-926A-512
12	52	18.4	716	6	US-10-127-829A-512
13	52	18.4	716	6	US-10-127-831A-512
14	52	18.4	716	6	US-10-127-835A-512
15	52	18.4	716	6	US-10-127-837A-512
16	52	18.4	716	6	US-10-127-842A-512
17	52	18.4	716	6	US-10-127-850A-512
18	52	18.4	716	6	US-10-127-901A-512
19	52	18.4	716	6	US-10-128-689A-512
20	52	18.4	716	6	US-10-131-830A-512
21	52	18.4	716	6	US-10-131-833A-512
22	52	18.4	716	6	US-10-131-837A-512
23	52	18.4	716	6	US-10-125-930A-512
24	52	18.4	716	6	US-10-127-825A-512
25	52	18.4	716	6	US-10-127-838B-512
26	52	18.4	716	6	US-10-127-843A-512

27	52	18.4	716	6	US-10-127-849A-512	Sequence 512, App
28	52	18.4	716	6	US-10-128-684A-512	Sequence 512, App
29	52	18.4	716	6	US-10-128-685A-512	Sequence 512, App
30	52	18.4	716	6	US-10-128-686A-512	Sequence 512, App
31	52	18.4	716	6	US-10-128-690A-512	Sequence 512, App
32	52	18.4	716	6	US-10-128-693A-512	Sequence 512, App
33	52	18.4	716	6	US-10-131-821A-512	Sequence 512, App
34	52	18.4	716	6	US-10-131-836A-512	Sequence 512, App
35	52	18.4	716	6	US-10-137-872A-512	Sequence 512, App
36	52	18.4	716	6	US-10-137-873A-512	Sequence 512, App
37	52	18.4	716	6	US-10-125-921A-512	Sequence 512, App
38	52	18.4	716	6	US-10-125-928A-512	Sequence 512, App
39	52	18.4	716	6	US-10-127-821A-512	Sequence 512, App
40	52	18.4	716	6	US-10-127-822A-512	Sequence 512, App
41	52	18.4	716	6	US-10-127-824A-512	Sequence 512, App
42	52	18.4	716	6	US-10-127-827A-512	Sequence 512, App
43	52	18.4	716	6	US-10-127-830A-512	Sequence 512, App
44	52	18.4	716	6	US-10-127-832A-512	Sequence 512, App
45	52	18.4	716	6	US-10-127-834A-512	Sequence 512, App

#### ALIGNMENTS

##### RESULT 1

US-10-092-411A-4480  
; Sequence 4480, Application US/10092411A  
; GENERAL INFORMATION:

; APPLICANT: Lynn Doucette-Stamm et al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC

; FILE REFERENCE: 032796-101

; CURRENT APPLICATION NUMBER: US/10/092,411A

; CURRENT FILING DATE: 2002-03-07

; PRIOR APPLICATION NUMBER: US 09/134,001

; PRIOR FILING DATE: 1998-08-13

; PRIOR APPLICATION NUMBER: US 60/064,964

; PRIOR FILING DATE: 1997-11-08

; PRIOR APPLICATION NUMBER: US 60/055,779

; PRIOR FILING DATE: 1997-08-14

; NUMBER OF SEQ ID NOS: 5676

; SEQ ID NO 4480

; LENGTH: 673

; TYPE: PRT

; ORGANISM: Staphylococcus epidermidis

; US-10-092-411A-4480

Query Match 20.7%; Score 58.5; DB 6; Length 673;  
Best Local Similarity 32.3%; Pred. No. 3.1;  
Matches 20; Conservative 7; Mismatches 14; Indels 21; Gaps 4;

QY 6 RHVL-----GIGLIVLK---NLVFNHNSMYPSPKLS-----FQEAFLFFLL 46  
Db 21 RHIVPFISVILFGIEVILSLTNTNYF--NEHHPKLSAIIIGIVMTMLLFILY 78  
QY 47 KN 48  
Db 79 AN 80

##### RESULT 2

US-10-264-237-1435

; Sequence 1435, Application US/10264237

; GENERAL INFORMATION:

; APPLICANT: Birse et al.

; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

; FILE REFERENCE: PA131PI

; CURRENT APPLICATION NUMBER: US/10/264,237

; CURRENT FILING DATE: 2002-10-04

; PRIOR APPLICATION NUMBER: PCT/US01/16450

; PRIOR FILING DATE: 2001-05-18

; PRIOR APPLICATION NUMBER: US 60/205,515

; PRIOR FILING DATE: 2000-05-19





22

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; APPLICANT: Wood,William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C138
; CURRENT APPLICATION NUMBER: US/10/131,829A
; CURRENT FILING DATE: 2002-04-27
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 512
; LENGTH: 716
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-131-829A-512

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Query Match 18.4%; Score 52; DB 6; Length 716;
Best Local Similarity 32.5%; Pred. No. 24;
Matches 13; Conservative 10; Mismatches 17; Indels 0; Gaps 0;

QY 11 IGLIVLKNLYFHKNMYPSPKLSFQEAFLFFFLILKNPL 50
Db 236 VGLDSLESFYDNKLVKVPQALQKVPNLFKFLDNKNPI 275

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RESULT 11
US-10-125-926A-512
; Sequence 512, Application US/10125926A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C80
; CURRENT APPLICATION NUMBER: US/10/125,926A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974

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; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
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; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 512
; LENGTH: 716
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-125-926A-512

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Query Match 18.4%; Score 52; DB 6; Length 716;
Best Local Similarity 32.5%; Pred. No. 24;
Matches 13; Conservative 10; Mismatches 17; Indels 0; Gaps 0;

QY 11 IGLIVLKNLYFHKNMYPSPKLSFQEAFLFFFLILKNPL 50
Db 236 VGLDSLESFYDNKLVKVPQALQKVPNLFKFLDNKNPI 275

RESULT 12
US-10-127-829A-512
; Sequence 512, Application US/10127829A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C85
; CURRENT APPLICATION NUMBER: US/10/127,829A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
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; PRIOR APPLICATION NUMBER: 60/059184

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; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 512
; LENGTH: 716
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-127-829A-512

Query Match      18.4%; Score 52; DB 6; Length 716;
Best Local Similarity 32.5%; Pred. No. 24;
Matches 13; Conservative 10; Mismatches 17; Indels 0; Gaps 0;

Oy 11 IGLIVLKNLYFHKNMYPSPKLSFQEAFLFFFLILKNPL 50
Db 236 VGLDSLESFYDNKLVKVPQLAQKVPNLKFLDLNKNPI 275

RESULT 13
US-10-127-831A-512
; Sequence 512, Application US/10127831A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330RIC107
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
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; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 512
; LENGTH: 716
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-127-829A-512

Query Match      18.4%; Score 52; DB 6; Length 716;
Best Local Similarity 32.5%; Pred. No. 24;
Matches 13; Conservative 10; Mismatches 17; Indels 0; Gaps 0;

Oy 11 IGLIVLKNLYFHKNMYPSPKLSFQEAFLFFFLILKNPL 50
Db 236 VGLDSLESFYDNKLVKVPQLAQKVPNLKFLDLNKNPI 275

RESULT 14
US-10-127-835A-512
; Sequence 512, Application US/10127835A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330RIC102
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
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; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 512
; LENGTH: 716
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-127-835A-512

Query Match      18.4%; Score 52; DB 6; Length 716;
Best Local Similarity 32.5%; Pred. No. 24;
Matches 13; Conservative 10; Mismatches 17; Indels 0; Gaps 0;

Oy 11 IGLIVLKNLYFHKNMYPSPKLSFQEAFLFFFLILKNPL 50
Db 236 VGLDSLESFYDNKLVKVPQLAQKVPNLKFLDLNKNPI 275
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Job time : 12 secs





GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 21, 2002, 13:40:48 ; Search time 18 Seconds  
(without alignments)  
288.403 Million cell updates/sec

Title: US-09-776-724A-142  
Perfect score: 283  
Sequence: 1 MRRCVRHVLGIGLVKLNLY.....FQEAFLFFLLKLNPLTCS 54

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR-73.\*

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2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	63	22.3	395	2 T09895	hypothetical prote
2	60	21.2	111	2 S64364	probable membrane
3	60	21.2	221	2 E69142	mannosyltransferas
4	58.5	20.7	394	2 T32214	hypothetical prote
5	58.5	20.7	612	2 T10727	protein kinase Xa2
6	57.5	20.3	170	2 AD0114	conserved hypotet
7	56.5	20.0	153	2 S64628	probable membrane
8	56.5	20.0	399	2 C49897	tryptophan synthas
9	56	19.8	177	2 T28263	ORF MSV102 hypotet
10	56	19.8	321	2 T27463	hypothetical prote
11	56	19.8	378	2 A55735	g protein-coupled
12	56	19.8	472	2 T51858	branched-chain alp
13	56	19.8	472	2 A86347	branched-chain alp
14	56	19.8	491	2 AC1185	B. subtilis ybtB p
15	56	19.8	494	2 AB1543	B. subtilis ybtB p
16	56	19.8	604	2 T44835	hypothetical prote
17	56	19.8	706	2 G72499	hypothetical prote
18	55.5	19.6	297	2 T26464	hypothetical prote
19	55.5	19.6	329	2 D69461	phosphoribosylform
20	55.5	19.6	363	2 T24731	hypothetical prote
21	55.5	19.6	385	2 A99807	glucans biosynthes
22	55.5	19.6	385	2 E85666	hypothetical prote
23	55.5	19.6	385	2 D64847	probable membrane
24	54.5	19.3	379	2 T04608	ADP,ATP carrier pr
25	54.5	19.3	379	2 S57971	aspartic proteinas
26	54.5	19.3	993	2 T25624	hypothetical prote
27	54.5	19.3	1757	2 T14318	ubiquitin-protein
28	54	19.1	277	2 D64666	glutamine ABC tran
29	54	19.1	554	2 T11267	NADH2 dehydrogenas

30	54	19.1	588	2 B71802	penicillin-binding
31	54	19.1	588	2 B64715	penicillin-binding
32	54	19.1	633	2 S49788	probable membrane
33	54	19.1	780	2 T03156	ribonucleoside-dip
34	54	19.1	1944	2 T40065	trna-splicing endo
35	53.5	18.9	397	2 C84078	hypothetical prote
36	53.5	18.9	2971	2 T08026	hypothetical prote
37	53	18.7	230	2 S09778	hypothetical prote
38	53	18.7	322	2 S35380	mcs2 protein - fis
39	53	18.7	386	2 T09709	ADP,ATP carrier pr
40	53	18.7	643	1 F0VZZW	major core protein
41	53	18.7	644	1 F0VZ5R	major core protein
42	53	18.7	644	2 T37390	major core protein
43	53	18.7	744	2 C90089	hypothetical prote
44	53	18.7	1694	2 Q01896	hypothetical 191.1
45	52.5	18.6	319	2 F81319	ADP-heptose-LPS he

## ALIGNMENTS

### RESULT 1

T09895

hypothetical protein T22A6.150 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 02-Sep-2000

C:Accession: T09895

R:Bevan, M.; Zimmermann, W.; Grueneisen, A.; Wambutt, R.; Bancroft, I.; Mewes, H.W.;

submitted to the Protein Sequence Database, June 1999

A:Reference number: Z16896

A:Accession: T09895

A:Molecule type: DNA

A:Residues: 1-395 <BEV>

A:Cross-references: EMBL:AL078637; GSPDB:GN00062; ATSP:T22A6.150

A:Experimental source: cultivar Columbia; BAC clone T22A6

C:Genetics:

A:Gene: ATSP:T22A6.150

A:Map position: 4

C:Superfamily: Arabidopsis thaliana hypothetical protein T20010.190

Query Match

Best Local Similarity

Matches

17; Conservative

8; Mismatches

22; Indels

4; Gaps

1;

QY 4 CVRHVGLGLIVLKNLYFHKNMYPSPKLSS-----FQEAFLFFLLKLNPL 50

DB 294 CLGEYLGFGMRFKKALVHHPGIFVMSHKIRQTQTVLVREAYHKVFLERHPL 344

### RESULT 2

S64364

probable membrane protein YGR069w - yeast (Saccharomyces cerevisiae)

N:Alternate names: hypothetical protein G4554

C:Species: Saccharomyces cerevisiae

C>Date: 17-May-1996 #sequence\_revision 17-May-1996 #text\_change 19-Apr-2002

C:Accession: S64364

R:Wedler, H.; Scharfe, M.; Wedler, E.; Wambutt, R.

submitted to the Protein Sequence Database, May 1996

A:Reference number: S64356

A:Accession: S64364

A:Molecule type: DNA

A:Residues: 1-111 <WED>

A:Cross-references: EMBL:Z72853; NID:gl323091; PID:gl323093; GSPDB:GN00007; MIPS:YGR0

C:Genetics:

A:Gene: MIPS:YGR069w

A:Cross-references: SGD:S0003301

A:Map position: 7R

C:Superfamily: Saccharomyces probable membrane protein YGR069w

C:Keywords: transmembrane protein

F:31-47/Domain: transmembrane #status predicted <TMM>

Query Match

21.2%; Score 60; DB 2; Length 111;

Best Local Similarity 34.0%; Pred. NO. 1.5;  
Matches 16; Conservative 5; Mismatches 20; Indels 6; Gaps 1;

4 CVRHVGIGLIVLKNLYHFKNSMPSKLSQFEAFLEFFFLILKNPL 50  
12 CTRFYL-----LLPSYTHNHLHFPPISIFSEFFFEFFFRNCL 52

QY  
DB

RESULT 3  
E919142  
mannosyltransferase - Methanobacterium thermoautotrophicum (strain Delta H)  
C:Species: Methanobacterium thermoautotrophicum  
C:date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 24-Nov-1999  
C:Accession: E919142  
R:Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;  
; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiواني, N.  
ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.  
J. Bacteriol. 179, 7135-7155, 1997  
A:title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct  
A:reference number: A69000; MUID:98037514; PMID:9371463  
A:Accession: E919142  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-221 <NTH>  
A:Cross-references: GB:AE000818; GB:AE000666; NID:g2621384; PIDN:AAB84837.1; PID:g262138  
A:Experimental source: strain Delta H  
C:Genetics:  
A:Gene: MTH331  
A:Start codon: GTG  
A:Start frequency: Methanobacterium thermoautotrophicum dolichyl-phosphate mannose synthase

```

Query Match          21.2%; Score 60; DB 2; Length 221;
Best Local Similarity 30.9%; Pred. No. 3,2;
Matches 21; Conservative 8; Mismatches 15; Indels 24; Gaps 3;

          2 RRCVRHVLIGL-----IVLKNLYFHKNMYPSPKLSGFOEAF- 39
          || :||: ||
Db 153 RRAIHLEELNGYSGFELEAEFMSKLARAGLKIVPTIYRRRS--DEPKLSSTFDGFK 210

          QY 40 LFFFLILK 47
          :| :| :|
Db 211 IFTLVLE 218

```

RESULT 4

T32214

hypothetical protein T03D3.10 - *Caenorhabditis elegans*

C:Species: *Caenorhabditis elegans*

C:Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 29-Oct-1999

C:Accession: T32214

R:Murray, J.; Wohldmann, P.; Bauer, C.; Biewald, T.

submitted to the EMBL Data Library, September 1997

A:Description: The sequence of *C. elegans* cosmid T03D3.

A:Reference number: 221136

A:Accession: T32214

A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-394 <MUR>

A:Cross-references: EMBL:AF022980; PIDN:AAB69921.1; GSPDB:GN00023; CESP:T03D3.10

A:Experimental source: strain Bristol NZ; clone T03D3

C:Genetics:

A:Gene: CESP:T03D3.10

A:Map position: 5

A:Map position: 235/3; 269/3; 326/2

```

Query Match      20.7%  SCORE 58.5;  DB 2;  Length 394;
Best Local Similarity 30.8%  Pred. No. 9;
Matches 16;  Conservative 11;  Mismatches 18;  Indels 7;  Gaps 3;

      6 RHVIGIGLVLKNIYF-HKNSMTPSKLSFQ--EAFLEFFFLIKNPITLCS 54
      11111111111111111111111111111111111111111111111111111
      20 RHILVIGILLSEVLAKQTFYENTRTQFMLEDWIYLYL---PTFCA 67

```

**RESULT 5**

Tt10727  
protein kinase Xa21 (EC 2.7.1.-) D, receptor type - long-staminate rice  
C:Species: Oryza longistaminata (long-staminate rice)  
C:Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 21-Jul-2000  
C:Accession: Tt10727  
R:Song, W.Y.; Pi, L.Y.; Wang, G.L.; Gardner, J.; Holsten, T.; Ronald, P.C.  
Plant Cell 9, 1279-1287, 1997  
A>Title: Evolution of the rice xa21 disease resistance gene family.  
A:Reference number: 215276; MUID:97432142; PMID:9286106  
A:Accession: Tt10727  
A>Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-612 <SON>  
A:Cross-references: EMBL:U72726; NID:g2586078; PIDN:AAB82753.1; PID:g2586081  
A:Experimental source: strain IRBB21  
C:Genetics:  
A:Map position: 11  
C:Keywords: phosphotransferase

	Query Match	20.7%	Score 58.5;	DB 2;	Length 612;	
	Best Local Similarity	38.3%;	Pred. No. 14;			
	Matches 18;	Conservative	5;	Mismatches 19;	Indels 5;	Gaps 2;

QY 1 MRRCRVHVLGIGLVILKNLYFKHKSM---YPSP--KLSSFOCAFLEF 42  
          :-: : : | | | | | : | | : | | : | | : |  
DB 163 LRGMIPREIGASLKHLKSLNLYLKHNGLSGEIPSAIGNLTSLDFFDLSF 209  
          :-: : : | | | | | : | | : | | : | | : |

**RESULT 6**

AD0114  
conserved hypothetical protein YPO0932 [imported] - Yersinia pestis (strain CO92)  
C:Species: Yersinia pestis  
C:Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 09-Nov-2001  
C:Accession: AD0114  
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice,  
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan,  
M.; Karpman, S.; Kell, D.; Kingsley, M.A.; Kitchin, I.; Landra, P.; Littlewood, J.K.;  
M., M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Ba-  
Nure, A.I.; 523-527, 2001  
A>Title: Genome sequence of Yersinia pestis, the causative agent of plague.  
A:Reference number: AB0001; MUID:21470413; PMID:11586360  
A:Accession: AD0114  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-170 <KUR>  
A:Cross-references: GB:AL590842; PIDN:CAC89775.1; PID:g15979002; GSPDB:GN00175  
C:Genetics:  
A:Gene: YPO0932  
C:Superfamily: hypothetical protein H1173

	Query Match	20.3%;	Score 57.5;	DB 2;	Length 170;	
	Best Local Similarity	30.4%;	Pred. No. 5.1;			
	Matches 17;	Conservative	8;	Mismatches 18;	Indels 13;	Gaps 2;

QY 3 RCVRHVVLGIGLVILKNLYFKHKSMYPKLSLFQ-----EAFLLFLIKNPDLTL 52  
          :-: | | | | | : | | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : |  
DB 16 QCLRHLQLTA-----NQHLGTAYPEPKVNHORGTNAGSAYLQSFEIRLNPLVL 64  
          :-: | | | | | : | | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : |

**RESULT 7**

S64628  
probable membrane protein YGR293c - yeast (Saccharomyces cerevisiae)  
A:Alternate names: hypothetical protein G9596  
C:Species: Saccharomyces cerevisiae  
C:Date: 17-May-1996 #sequence\_revision 17-May-1996 #text\_change 19-Apr-2002  
C:Accession: S64628; S64630  
R:Voet, M.; Voickaert, G. Sequence Database, May 1996  
submitted to the Protein Sequence Database, May 1996  
A:Reference number: S64611  
A:Accession: S64628  
A:Molecule type: DNA  
A:Residues: 1-153 <VOE>

J. Virol. 73, 533-552, 1999

A:Title: The genome of Melanoplus sanguinipes entomopoxvirus.

A:Reference number: Z20484; MUID:99102612; PMID:9847359

A:Accession: T28263

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-177 <AFO>

A:Cross-references: EMBL:AF053866; NID:g4049647; PIDN:AAC97649.1; PID:g4049689

C:Genetics:

A:Note: MSV102

Query Match 19.8%; Score 56; DB 2; Length 177;

Best Local Similarity 36.4%; Pred. No. 8.3;

Matches 12; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

QY 18 NLYFHKNMYPSPKLSFQEAFLFFFLILKNPL 50

DB 137 DLIFCKNIIINPTNNYKKALNFYFLDKKNL 169

RESULT 10

T27463

hypothetical protein Y87G2A.k - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999

C:Accession: T27463

R:White, S.

A:submitted to the EMBL Data Library, September 1999

A:Reference number: Z20371

A:Accession: T27463

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-321 <WIL>

A:cross-references: EMBL:AL110500; NID:e1542314; PIDN:CAB54485.1; CESP:Y87G2A

A:Experimental source: clone Y87G2A

C:Genetics:

A:Gene: CESP:Y87G2A.k

A:introns: 29/1; 89/1; 189/1; 299/3

Query Match 19.8%; Score 56; DB 2; Length 321;

Best Local Similarity 32.4%; Pred. No. 15;

Matches 11; Conservative 5; Mismatches 18; Indels 0; Gaps 0;

QY 17 KNLYFHKNMYPSPKLSFQEAFLFFFLILKNPL 50

DB 7 KKLFFHNGKPPKTKFFKTKQILYFNKKNP 40

RESULT 11

A55735

G protein-coupled receptor EB11 - mouse

C:Species: Mus musculus (house mouse)

C:Date: 07-Jul-1995 #sequence\_revision 07-Jul-1995 #text\_change 24-Nov-1999

C:Accession: A55735

R:Schweikart, V.L.; Raport, C.J.; Godiska, R.; Byers, M.G.; Eddy Jr., R.L.; S.

Genomics 23, 643-650, 1994

A:Title: Cloning of human and mouse EB11, a lymphoid-specific G-protein-coupled receptor

A:Reference number: A55735; MUID:95154835; PMID:7851893

A:Accession: A55735

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-378 <SCH>

A:Cross-references: GB:I31580; NID:g468340; PIDN:AAA74232.1; PID:g468341

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor

Query Match 19.8%; Score 56; DB 2; Length 378;

Best Local Similarity 32.6%; Pred. No. 18;

Matches 14; Conservative 7; Mismatches 22; Indels 0; Gaps 0;

QY 4 CVRVLGIGLIVLKNLYFHKNMYPSPKLSFQEAFLFFFLIL 46

DB 69 CFVGLGNGLIVLYYFKRLKMTDTYILNLAVADILFLIL 111



GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 21, 2002, 13:42:31 ; Search time 10 Seconds  
(without alignments)  
84.572 Million cell updates/sec

Title: US-09-776-724A-142

Perfect score: 283

Sequence: 1 MRRCVRHVIGLIVLNXY.....FOEAFLEFFLLKNPLTLC 54

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 100480 seqs, 15661496 residues

Total number of hits satisfying chosen parameters: 100480

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published\_Applications\_AA:\*

1: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB pep: \*  
2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB pep: \*  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB pep: \*  
4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB pep: \*  
5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB pep: \*  
6: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB pep: \*  
7: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB pep: \*  
8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB pep: \*  
9: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB pep: \*  
10: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB pep: \*  
11: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB pep: \*  
12: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB pep: \*  
13: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB pep: \*  
14: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB pep: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Query Match	Score	Length	DB ID	Description
1	59	20.8	260	10	US-09-761-288-35
2	59	20.8	260	10	US-09-761-288-35
3	59	20.8	304	10	US-09-747-835A-58
4	59	20.8	310	10	US-09-761-288-4
5	59	20.8	310	10	US-09-761-288-38
6	59	20.8	310	10	US-09-761-288-67
7	59	20.8	310	10	US-09-761-288-89
8	58.5	20.7	612	8	US-08-910-386A-2
9	55.5	19.6	91	12	US-10-001-879-160
10	52.5	18.6	96	10	US-09-925-301-1300
11	52.5	18.6	216	10	US-09-745-763-4
12	52.5	18.6	1025	8	US-08-910-386A-7
13	52	18.4	310	10	US-09-761-288-22
14	52	18.4	310	10	US-09-761-288-24
15	52	18.4	310	10	US-09-761-288-64
16	52	18.4	372	10	US-09-804-156-15
17	52	18.4	372	10	US-09-946-633-7
18	52	18.4	384	9	US-09-945-249-8
19	52	18.4	714	10	US-09-803-589-7
					Sequence 35, Appl
					Sequence 36, Appl
					Sequence 58, Appl
					Sequence 4, Appl
					Sequence 38, Appl
					Sequence 67, Appl
					Sequence 89, Appl
					Sequence 2, Appl
					Sequence 160, Appl
					Sequence 1300, Appl
					Sequence 4, Appl
					Sequence 7, Appl
					Sequence 22, Appl
					Sequence 24, Appl
					Sequence 64, Appl
					Sequence 15, Appl
					Sequence 7, Appl
					Sequence 8, Appl
					Sequence 7, Appl

20	51.5	18.2	318	10	US-09-801-368-252	Sequence 252, Appl
21	51	18.0	193	10	US-09-815-242-4983	Sequence 4983, Appl
22	51	18.0	206	10	US-09-811-284-189	Sequence 189, Appl
23	50.5	17.8	63	10	US-09-864-761-37449	Sequence 37449, Appl
24	50	17.7	103	10	US-09-764-864-1448	Sequence 1448, Appl
25	50	17.7	160	10	US-09-764-864-1020	Sequence 1020, Appl
26	50	17.7	189	10	US-09-764-878-162	Sequence 162, Appl
27	50	17.5	655	10	US-09-815-242-13946	Sequence 13946, Appl
28	49.5	17.5	96	10	US-09-905-243-11	Sequence 11, Appl
29	49	17.3	66	10	US-09-764-887-265	Sequence 265, Appl
30	49	17.3	117	9	US-09-949-842-17	Sequence 17, Appl
31	49	17.3	315	10	US-09-978-249-9	Sequence 9, Appl
32	49	17.3	413	10	US-09-771-161A-178	Sequence 178, Appl
33	49	17.3	422	10	US-09-771-161A-269	Sequence 269, Appl
34	49	17.3	422	10	US-09-771-161A-270	Sequence 270, Appl
35	49	17.3	426	9	US-09-909-650A-24	Sequence 24, Appl
36	49	17.3	541	12	US-10-047-676A-11	Sequence 11, Appl
37	49	17.3	581	12	US-10-139-876-18	Sequence 18, Appl
38	49	17.3	837	12	US-10-052-586-454	Sequence 454, Appl
39	48.5	17.1	292	10	US-09-886-055-315	Sequence 315, Appl
40	48.5	17.1	313	10	US-09-886-055-115	Sequence 115, Appl
41	48.5	17.1	700	10	US-09-841-132-345	Sequence 345, Appl
42	48.5	17.1	1751	10	US-09-841-132-445	Sequence 445, Appl
43	48.5	17.1	1751	10	US-09-841-132-594	Sequence 594, Appl
44	48.5	17.1	1752	10	US-09-841-132-180	Sequence 180, Appl
45	48	17.0	105	10	US-09-740-668A-44	Sequence 44, Appl

#### ALIGNMENTS

#### RESULT 1

US-09-761-288-35  
; Sequence 35, Application US/09761288  
; Patent No. US20020065405A1  
; GENERAL INFORMATION:  
; APPLICANT: Padigaru, Muralidhara  
; APPLICANT: Prayaga, Sudhirdas  
; APPLICANT: Taupier, Raymond J  
; APPLICANT: Mishra, Vishnu  
; APPLICANT: Tchernev, Velizar  
; APPLICANT: Spyttek, Kimberly  
; APPLICANT: Li, Li  
; TITLE OF INVENTION: No. US20020065405A1 Polypeptides and Nucleic Acids Encoding  
; FILE REFERENCE: 15966-638  
; CURRENT APPLICATION NUMBER: US/09761,288  
; CURRENT FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: 60/177,839  
; PRIOR FILING DATE: 2000-01-25  
; PRIOR APPLICATION NUMBER: 60/176,134  
; PRIOR FILING DATE: 2000-01-14  
; PRIOR APPLICATION NUMBER: 60/175,989  
; PRIOR FILING DATE: 2000-01-13  
; PRIOR APPLICATION NUMBER: 60/218,324  
; PRIOR FILING DATE: 2000-07-14  
; PRIOR APPLICATION NUMBER: 60/220,253  
; PRIOR FILING DATE: 2000-07-24  
; PRIOR APPLICATION NUMBER: 60/178,191  
; PRIOR FILING DATE: 2000-01-26  
; PRIOR APPLICATION NUMBER: 60/178,227  
; PRIOR FILING DATE: 2000-01-26  
; PRIOR APPLICATION NUMBER: 60/220,590  
; PRIOR FILING DATE: 2000-07-25  
; NUMBER OF SEQ ID NOS: 95  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 35  
; LENGTH: 260  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: (152)..(165)  
; OTHER INFORMATION: Wherein Xaa is any amino acid.

US-09-761-288-35

Query Match 20.8%; Score 59; DB 10; Length 260;  
Best Local Similarity 30.4%; Pred. No. 1.2;  
Matches 17; Conservative 9; Mismatches 24; Indels 6; Gaps 2;

QY 2 RRCVRHVLGIGLIVLKNLYFHKNMYPSPKLSFQAEFLFFFLILKNPL---TLCS 54  
| | | | | : : : : : | : : | | | | | : : : : :  
Db 188 RTCFSLVCLVGLVGTATIMVGPYGNPK---EQKKYLLLFHSLFNPMLNPLICS 240

RESULT 2

US-09-761-288-36  
; Sequence 36, Application US/09761288  
; Patent No. US20020065405A1  
; GENERAL INFORMATION:  
; APPLICANT: Padigar, Muralidhara  
; APPLICANT: Prayaga, Sudhirdas  
; APPLICANT: Taupier, Raymond J  
; APPLICANT: Mishra, Vishnu  
; APPLICANT: Tchernev, Velizar  
; APPLICANT: Spytek, Kimberky  
; APPLICANT: Li, Li  
; TITLE OF INVENTION: No. US20020065405A1el Polypeptides and Nucleic Acids Encoding Sam  
; FILE REFERENCE: 15966-638  
; CURRENT APPLICATION NUMBER: US/09761,288  
; CURRENT FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: 60/177,839  
; PRIOR FILING DATE: 2000-01-25  
; PRIOR APPLICATION NUMBER: 60/176,134  
; PRIOR FILING DATE: 2000-01-14  
; PRIOR APPLICATION NUMBER: 60/175,989  
; PRIOR FILING DATE: 2000-01-13  
; PRIOR APPLICATION NUMBER: 60/218,324  
; PRIOR FILING DATE: 2000-07-14  
; PRIOR APPLICATION NUMBER: 60/220,253  
; PRIOR FILING DATE: 2000-07-24  
; PRIOR APPLICATION NUMBER: 60/178,191  
; PRIOR FILING DATE: 2000-01-26  
; PRIOR APPLICATION NUMBER: 60/178,227  
; PRIOR FILING DATE: 2000-01-26  
; PRIOR APPLICATION NUMBER: 60/220,590  
; PRIOR FILING DATE: 2000-07-25  
; NUMBER OF SEQ ID NOS: 95  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 36  
; LENGTH: 260  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-761-288-36

Query Match 20.8%; Score 59; DB 10; Length 260;  
Best Local Similarity 30.4%; Pred. No. 1.2;  
Matches 17; Conservative 9; Mismatches 24; Indels 6; Gaps 2;

QY 2 RRCVRHVLGIGLIVLKNLYFHKNMYPSPKLSFQAEFLFFFLILKNPL---TLCS 54  
| | | | | : : : : : | : : | | | | | : : : : :  
Db 188 RTCFSLVCLVGLVGTATIMVGPYGNPK---EQKKYLLLFHSLFNPMLNPLICS 240

RESULT 3

US-09-747-835A-58  
; Sequence 58, Application US/09747835A  
; Patent No. US20020146692A1  
; GENERAL INFORMATION:  
; APPLICANT: Yamazaki, Victoria  
; APPLICANT: Tang, Y. Tom  
; APPLICANT: Liu, Chenghua  
; APPLICANT: Zhou, Ping  
; APPLICANT: Wang, Dunrui  
; APPLICANT: Zhang, Jie  
; APPLICANT: Ren, Feiyan  
; APPLICANT: Asundi, Vinod

; APPLICANT: Drmanac, Radoje T  
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO G PROTEIN-COUPLED RECEPTOR-L  
; FILE REFERENCE: HYS-37CIP  
; CURRENT APPLICATION NUMBER: US/09/747,835A  
; CURRENT FILING DATE: 2002-03-08  
; PRIOR APPLICATION NUMBER: US 09/729,739  
; PRIOR FILING DATE: 2000-12-04  
; PRIOR APPLICATION NUMBER: US 09/653,450  
; PRIOR FILING DATE: 2000-08-31  
; PRIOR APPLICATION NUMBER: US 09/620,312  
; PRIOR FILING DATE: 2000-07-19  
; PRIOR APPLICATION NUMBER: US 09/598,042  
; PRIOR FILING DATE: 2000-06-20  
; PRIOR APPLICATION NUMBER: US 09/552,317  
; PRIOR FILING DATE: 2000-04-25  
; PRIOR APPLICATION NUMBER: US 09/488,725  
; PRIOR FILING DATE: 2000-01-21  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 58  
; LENGTH: 304  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-747-835A-58

Query Match 20.8%; Score 59; DB 10; Length 304;  
Best Local Similarity 30.4%; Pred. No. 1.4;  
Matches 17; Conservative 9; Mismatches 24; Indels 6; Gaps 2;

QY 2 RRCVRHVLGIGLIVLKNLYFHKNMYPSPKLSFQAEFLFFFLILKNPL---TLCS 54  
| | | | | : : : : : | : : | | | | | : : : : :  
Db 238 RTCFSLVCLVGLVGTATIMVGPYGNPK---EQKKYLLLFHSLFNPMLNPLICS 290

RESULT 4

US-09-761-288-4  
; Sequence 4, Application US/09761288  
; Patent No. US20020065405A1  
; GENERAL INFORMATION:  
; APPLICANT: Padigar, Muralidhara  
; APPLICANT: Prayaga, Sudhirdas  
; APPLICANT: Taupier, Raymond J  
; APPLICANT: Mishra, Vishnu  
; APPLICANT: Tchernev, Velizar  
; APPLICANT: Spytek, Kimberky  
; APPLICANT: Li, Li  
; TITLE OF INVENTION: No. US20020065405A1el Polypeptides and Nucleic Acids Encoding  
; FILE REFERENCE: 15966-638  
; CURRENT APPLICATION NUMBER: US/09/761,288  
; CURRENT FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: 60/177,839  
; PRIOR FILING DATE: 2000-01-25  
; PRIOR APPLICATION NUMBER: 60/176,134  
; PRIOR FILING DATE: 2000-01-14  
; PRIOR APPLICATION NUMBER: 60/175,989  
; PRIOR FILING DATE: 2000-01-13  
; PRIOR APPLICATION NUMBER: 60/218,324  
; PRIOR FILING DATE: 2000-07-14  
; PRIOR APPLICATION NUMBER: 60/220,253  
; PRIOR FILING DATE: 2000-07-24  
; PRIOR APPLICATION NUMBER: 60/178,191  
; PRIOR FILING DATE: 2000-01-26  
; PRIOR APPLICATION NUMBER: 60/178,227  
; PRIOR FILING DATE: 2000-01-26  
; PRIOR APPLICATION NUMBER: 60/220,590  
; PRIOR FILING DATE: 2000-07-25  
; NUMBER OF SEQ ID NOS: 95  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 310  
; TYPE: PRT  
; ORGANISM: Homo sapiens

US-09-761-288-4

Query Match 20.8%; Score 59; DB 10; Length 310;  
Best Local Similarity 30.4%; Pred. No. 1.5;  
Matches 17; Conservative 9; Mismatches 24; Indels 6; Gaps 2;

QY 2 RRCRVHVLGIGLVKLVNLFHKNMYPSPKLSFQEAFLFFFLIKNPL---TLCS 54  
| | | : | | : : : | : | | : | | : | | : | | : | |  
Db 238 RTCFSLCVLIGLVGTATIMYVGPYGNPK---EQKKYLLHLSLFPNMLNPLICS 290

RESULT 5

US-09-761-288-38  
; Sequence 38, Application US/09761288  
; Patent No. US20020065405A1

; GENERAL INFORMATION:  
; APPLICANT: Padigaru, Muralidhara

; APPLICANT: Prayaga, Sudhirdas

; APPLICANT: Taupier, Raymond J

; APPLICANT: Mishra, Vishnu

; APPLICANT: Tchernev, Velizar

; APPLICANT: Spytek, Kimberly

; APPLICANT: Li, Li

; TITLE OF INVENTION: No. US20020065405A1el Polypeptides and Nucleic Acids Encoding Sam

; FILE REFERENCE: 15966-638

; CURRENT APPLICATION NUMBER: US/09/761,288

; CURRENT FILING DATE: 2001-01-16

; PRIOR APPLICATION NUMBER: 60/177,839

; PRIOR FILING DATE: 2000-01-25

; PRIOR APPLICATION NUMBER: 60/176,134

; PRIOR FILING DATE: 2000-01-14

; PRIOR APPLICATION NUMBER: 60/175,989

; PRIOR FILING DATE: 2000-01-13

; PRIOR APPLICATION NUMBER: 60/218,324

; PRIOR FILING DATE: 2000-07-14

; PRIOR APPLICATION NUMBER: 60/220,253

; PRIOR FILING DATE: 2000-07-24

; PRIOR APPLICATION NUMBER: 60/178,191

; PRIOR FILING DATE: 2000-01-26

; PRIOR APPLICATION NUMBER: 60/178,227

; PRIOR FILING DATE: 2000-01-26

; PRIOR APPLICATION NUMBER: 60/220,590

; PRIOR FILING DATE: 2000-07-25

; NUMBER OF SEQ ID NOS: 95

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 38

; LENGTH: 310

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-09-761-288-38

Query Match 20.8%; Score 59; DB 10; Length 310;

Best Local Similarity 30.4%; Pred. No. 1.5;

Matches 17; Conservative 9; Mismatches 24; Indels 6; Gaps 2;

QY 2 RRCRVHVLGIGLVKLVNLFHKNMYPSPKLSFQEAFLFFFLIKNPL---TLCS 54  
| | | : | | : : : | : | | : | | : | | : | | : | |  
Db 238 RTCFSLCVLIGLVGTATIMYVGPYGNPK---EQKKYLLHLSLFPNMLNPLICS 290

RESULT 6

US-09-761-288-67  
; Sequence 67, Application US/09761288  
; Patent No. US20020065405A1

; GENERAL INFORMATION:

; APPLICANT: Padigaru, Muralidhara

; APPLICANT: Prayaga, Sudhirdas

; APPLICANT: Taupier, Raymond J

; APPLICANT: Mishra, Vishnu

; APPLICANT: Tchernev, Velizar

; APPLICANT: Spytek, Kimberly

; APPLICANT: Li, Li

; TITLE OF INVENTION: No. US20020065405A1el Polypeptides and Nucleic Acids Encoding Sam

; FILE REFERENCE: 15966-638

; CURRENT APPLICATION NUMBER: US/09/761,288

; CURRENT FILING DATE: 2001-01-16

; PRIOR APPLICATION NUMBER: 60/177,839

; PRIOR FILING DATE: 2000-01-25

; PRIOR APPLICATION NUMBER: 60/176,134

; PRIOR FILING DATE: 2000-01-14

; PRIOR APPLICATION NUMBER: 60/175,989

; PRIOR FILING DATE: 2000-01-13

; PRIOR APPLICATION NUMBER: 60/218,324

; PRIOR FILING DATE: 2000-07-14

; PRIOR APPLICATION NUMBER: 60/220,253

; PRIOR FILING DATE: 2000-07-24

; PRIOR APPLICATION NUMBER: 60/178,191

; PRIOR FILING DATE: 2000-01-26

; PRIOR APPLICATION NUMBER: 60/178,227

; PRIOR FILING DATE: 2000-01-26

; PRIOR APPLICATION NUMBER: 60/220,590

; PRIOR FILING DATE: 2000-07-25

; NUMBER OF SEQ ID NOS: 95

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 67

; LENGTH: 310

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-09-761-288-67

Query Match 20.8%; Score 59; DB 10; Length 310;

Best Local Similarity 30.4%; Pred. No. 1.5;

Matches 17; Conservative 9; Mismatches 24; Indels 6; Gaps 2;

QY 2 RRCRVHVLGIGLVKLVNLFHKNMYPSPKLSFQEAFLFFFLIKNPL---TLCS 54  
| | | : | | : : : | : | | : | | : | | : | | : | |

Db 238 RTCFSLCVLIGLVGTATIMYVGPYGNPK---EQKKYLLHLSLFPNMLNPLICS 290  
| | | : | | : : : | : | | : | | : | | : | | : | |

RESULT 7

US-09-761-288-89

; Sequence 89, Application US/09761288

; Patent No. US20020065405A1

; GENERAL INFORMATION:

; APPLICANT: Padigaru, Muralidhara

; APPLICANT: Prayaga, Sudhirdas

; APPLICANT: Taupier, Raymond J

; APPLICANT: Mishra, Vishnu

; APPLICANT: Tchernev, Velizar

; APPLICANT: Spytek, Kimberly

; APPLICANT: Li, Li

; TITLE OF INVENTION: No. US20020065405A1el Polypeptides and Nucleic Acids Encoding

; FILE REFERENCE: 15966-638

; CURRENT APPLICATION NUMBER: US/09/761,288

; CURRENT FILING DATE: 2001-01-16

; PRIOR APPLICATION NUMBER: 60/177,839

; PRIOR FILING DATE: 2000-01-25

; PRIOR APPLICATION NUMBER: 60/176,134

; PRIOR FILING DATE: 2000-01-14

; PRIOR APPLICATION NUMBER: 60/175,989

; PRIOR FILING DATE: 2000-01-13

; PRIOR APPLICATION NUMBER: 60/218,324

; PRIOR FILING DATE: 2000-07-14

; PRIOR APPLICATION NUMBER: 60/220,253

; PRIOR FILING DATE: 2000-07-24

; PRIOR APPLICATION NUMBER: 60/178,191

; PRIOR FILING DATE: 2000-01-26

; PRIOR APPLICATION NUMBER: 60/178,227

; PRIOR FILING DATE: 2000-01-26

; PRIOR APPLICATION NUMBER: 60/220,590

; PRIOR FILING DATE: 2000-07-25

; NUMBER OF SEQ ID NOS: 95

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 89

; LENGTH: 310

; TYPE: PRT

```

; APPLICANT: Cafferkey, Robert
; APPLICANT: Ali, Shujath
; APPLICANT: Sun, Yongming
; APPLICANT: Liu, Chenghua
; TITLE OF INVENTION: Compositions and Methods Relating to Prostate Specific Genes a
; FILE REFERENCE: DEX-0281
; CURRENT APPLICATION NUMBER: US/10/001,879
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/252,188
; PRIOR FILING DATE: 2000-11-21
; NUMBER OF SEQ ID NOS: 201
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 160
; LENGTH: 91
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-001-879-160

Query Match 19.6%; Score 55.5; DB 12; Length 91;
Best Local Similarity 38.5%; Pred. No. 1.1;
Matches 15; Conservative 7; Mismatches 12; Indels 5; Gaps 2;

QY 14 IVLKNLYPHKNSMYPKLSFQEAFLFFFLILKNPLTL 52
      :||| :|| :|| :|| :|| :|| :|| :||
Ddb 58 VVIHFLYFT--LIPSKSLTS--ATFIFFLLHLHPCCFL 91

RESULT 10
US-09-925-301-1300
; Sequence 1300, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA106
; CURRENT APPLICATION NUMBER: US/09/925,301
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1300
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-301-1300

Query Match 18.6%; Score 52.5; DB 10; Length 96;
Best Local Similarity 35.0%; Pred. No. 2.8;
Matches 14; Conservative 5; Mismatches 16; Indels 5; Gaps 2;

QY 17 KNLYPHKNSMYPKLSFQEAFLFFFLILKNPLTL 53
      || :| | ||| :||| :||| :||| :|||
Ddb 18 KNCFLHPCGAYSSEPSQSQL--CFLFYFCIRFLLLLC 55

RESULT 11
US-09-745-763-4
; Sequence 4, Application US/09745763
; Patent No. US2002005394A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: LaVallie, Edward R.
; APPLICANT: Collins-Racie, Lisa A.
; APPLICANT: Evans, Cheryl
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Spaulding, Vikki
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
; ENCODING THEM

```



NUMBER OF SEQUENCES: 219  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genetics Institute, Inc.  
STREET: 87 Cambridgepark Drive  
CITY: Cambridge  
STATE: MA  
COUNTRY: U.S.A.  
ZIP: 02140  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/745,763  
FILING DATE: 18-Jun-2000  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Sprunger, Suzanne A.  
REGISTRATION NUMBER: 41,323  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 498-8284  
TELEFAX: (617) 876-5851  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 216 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-09-745-763-4

Query Match 18.6%; Score 52.5; DB 10; Length 216;  
Best Local Similarity 25.9%; Pred. No. 7;  
Matches 14; Conservative 14; Mismatches 21; Indels 5; Gaps 1;

QY 1 MRRCVRHVIGLVLKLYFKHNSMPSKLSFQEAFLFFLLKKNPLTCS 54  
DB 27 MATVCSILGVCLVMPINVEDNSL-----LNWKEAFGTMTVMAGLTALS 75

RESULT 12  
US-09-745-763-4  
Sequence 7, Application US/08910386A  
Patent No. US20020092041A1  
GENERAL INFORMATION:  
APPLICANT: Ronald, Pamela C.  
APPLICANT: Wang, Guo-Liang  
APPLICANT: Song, Wen-Yuang  
APPLICANT: Hulbert, Scott  
APPLICANT: Richter, Todd  
TITLE OF INVENTION: Procedures and Materials for Conferring  
TITLE OF INVENTION: Disease Resistance in Plants  
NUMBER OF SEQUENCES: 53  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/910,386A  
FILING DATE: 13-AUG-1997  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Bastian, Kevin L.

REGISTRATION NUMBER: 34,774  
REFERENCE/DOCKET NUMBER: 023070-0589500S  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1025 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-910-386A-7

Query Match 18.6%; Score 52.5; DB 8; Length 1025;  
Best Local Similarity 36.2%; Pred. No. 42;  
Matches 17; Conservative 6; Mismatches 19; Indels 5; Gaps 2;

QY 1 MRRCVRHVIGLVLKLYFKHNSM--YPSF--KLSSFQEAFLFF 42  
DB 163 LRGMIPREICASLKHLNLYKNGLSGEIPSAIENLTSIQEFDLSF 209

RESULT 13  
US-09-761-288-22  
Sequence 22, Application US/09761288  
Patent No. US20020065405A1  
GENERAL INFORMATION:  
APPLICANT: Padigaru, Muralidhara  
APPLICANT: Prayaga, Sudhirdas  
APPLICANT: Taupier, Raymond J  
APPLICANT: Mishra, Vishnu  
APPLICANT: Tchernev, Velizar  
APPLICANT: Spytek, Kimberky  
APPLICANT: Li, Li  
TITLE OF INVENTION: No. US20020065405A1el Polypeptides and Nucleic Acids Encoding  
FILE REFERENCE: 15966-638  
CURRENT APPLICATION NUMBER: US/09/761,288  
CURRENT FILING DATE: 2001-01-16  
PRIOR APPLICATION NUMBER: 60/177,839  
PRIOR FILING DATE: 2000-01-25  
PRIOR APPLICATION NUMBER: 60/176,134  
PRIOR FILING DATE: 2000-01-14  
PRIOR APPLICATION NUMBER: 60/175,989  
PRIOR FILING DATE: 2000-01-13  
PRIOR APPLICATION NUMBER: 60/218,324  
PRIOR FILING DATE: 2000-07-14  
PRIOR APPLICATION NUMBER: 60/220,253  
PRIOR FILING DATE: 2000-07-24  
PRIOR APPLICATION NUMBER: 60/178,191  
PRIOR FILING DATE: 2000-01-26  
PRIOR APPLICATION NUMBER: 60/178,227  
PRIOR FILING DATE: 2000-01-26  
PRIOR APPLICATION NUMBER: 60/220,590  
PRIOR FILING DATE: 2000-07-25  
NUMBER OF SEQ ID NOS: 95  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 22  
LENGTH: 310  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-761-288-22

Query Match 18.4%; Score 52; DB 10; Length 310;  
Best Local Similarity 29.6%; Pred. No. 12;  
Matches 16; Conservative 8; Mismatches 24; Indels 6; Gaps 2;

QY 4 CVRHVLGIGLVLKLYFKHNSMPSKLSFQEAFLFFLLKKNPL--TLCS 54  
DB 240 CFSHLCVIGLFGYGTAIMYGPYGNPK---EQKYLHLLHSLFNPMLNPICS 290

RESULT 14  
US-09-761-288-24

; Sequence 24, Application US/09761288  
; Patent No. US20020065405A1  
; GENERAL INFORMATION:  
; APPLICANT: Padigar, Muralidhara  
; APPLICANT: Prayaga, Sudhirdas  
; APPLICANT: Taupier, Raymond J  
; APPLICANT: Mishra, Vishnu  
; APPLICANT: Tchernev, Velizar  
; APPLICANT: Spytek, Kimberly  
; APPLICANT: Li, Li  
; TITLE OF INVENTION: NO. US20020065405A1el Polypeptides and Nucleic Acids Encoding Sam  
; FILE REFERENCE: 15966-638  
; CURRENT APPLICATION NUMBER: US/09/761,288  
; CURRENT FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: 60/177,839  
; PRIOR FILING DATE: 2000-01-25  
; PRIOR APPLICATION NUMBER: 60/176,134  
; PRIOR FILING DATE: 2000-01-14  
; PRIOR APPLICATION NUMBER: 60/175,989  
; PRIOR FILING DATE: 2000-01-13  
; PRIOR APPLICATION NUMBER: 60/218,324  
; PRIOR FILING DATE: 2000-07-14  
; PRIOR APPLICATION NUMBER: 60/220,253  
; PRIOR FILING DATE: 2000-07-24  
; PRIOR APPLICATION NUMBER: 60/178,191  
; PRIOR FILING DATE: 2000-01-26  
; PRIOR APPLICATION NUMBER: 60/178,227  
; PRIOR FILING DATE: 2000-01-26  
; PRIOR APPLICATION NUMBER: 60/220,590  
; PRIOR FILING DATE: 2000-07-25  
; NUMBER OF SEQ ID NOS: 95  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 24  
; LENGTH: 310  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-761-288-24

Query Match 18.4%; Score 52; DB 10; Length 310;  
Best Local Similarity 29.6%; Pred. No. 12;  
Matches 16; Conservative 8; Mismatches 24; Indels 6; Gaps 2;

QY 4 CVRHVLGIGLVLKNIYFKHKNMSPKLSQFAFLFFFLILKNPL---TLCS 54  
| | | | | : : | | | : | | | | | : | | : | |  
Db 240 CFSLCVIGLFGYGTAIMYVGPYGNPK---EQKKYLLLFHSLFNPMLNPLICS 290

## RESULT 15

US-09-761-288-64  
; Sequence 64, Application US/09761288  
; Patent No. US20020065405A1  
; GENERAL INFORMATION:  
; APPLICANT: Padigar, Muralidhara  
; APPLICANT: Prayaga, Sudhirdas  
; APPLICANT: Taupier, Raymond J  
; APPLICANT: Mishra, Vishnu  
; APPLICANT: Tchernev, Velizar  
; APPLICANT: Spytek, Kimberly  
; APPLICANT: Li, Li  
; TITLE OF INVENTION: NO. US20020065405A1el Polypeptides and Nucleic Acids Encoding Sam  
; FILE REFERENCE: 15966-638  
; CURRENT APPLICATION NUMBER: US/09/761,288  
; CURRENT FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: 60/177,839  
; PRIOR FILING DATE: 2000-01-25  
; PRIOR APPLICATION NUMBER: 60/176,134  
; PRIOR FILING DATE: 2000-01-14  
; PRIOR APPLICATION NUMBER: 60/175,989  
; PRIOR FILING DATE: 2000-01-13  
; PRIOR APPLICATION NUMBER: 60/218,324  
; PRIOR FILING DATE: 2000-07-14  
; PRIOR APPLICATION NUMBER: 60/220,253  
; PRIOR FILING DATE: 2000-07-24

; PRIOR APPLICATION NUMBER: 60/178,191  
; PRIOR FILING DATE: 2000-01-26  
; PRIOR APPLICATION NUMBER: 60/178,227  
; PRIOR FILING DATE: 2000-01-26  
; PRIOR APPLICATION NUMBER: 60/220,590  
; PRIOR FILING DATE: 2000-07-25  
; NUMBER OF SEQ ID NOS: 95  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 64  
; LENGTH: 310  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-761-288-64

Query Match 18.4%; Score 52; DB 10; Length 310;  
Best Local Similarity 29.6%; Pred. No. 12;  
Matches 16; Conservative 8; Mismatches 24; Indels 6; Gaps 2;

QY 4 CVRHVLGIGLVLKNIYFKHKNMSPKLSQFAFLFFFLILKNPL---TLCS 54  
| | | | | : : | | | : | | | | | : | | : | |  
Db 240 CFSLCVIGLFGYGTAIMYVGPYGNPK---EQKKYLLLFHSLFNPMLNPLICS 290

Search completed: November 21, 2002, 13:46:13  
Job time : 10 secs

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: November 21, 2002, 13:40:51 ; Search time 14 Seconds  
(without alignments)  
113.488 Million cell updates/sec

Title: US-09-776-724A-142

Perfect score: 283

Sequence: 1 MRCVHVHVLGILVILKNLY.....FOEAFLEFFLILKNPLTLC5 54

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_AA:\*

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2: /cgn2.6/prodata/1/1aa/5B\_COMB.pep:\*  
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5: /cgn2.6/prodata/1/1aa/PCTUS\_COMB.pep:\*  
6: /cgn2.6/prodata/1/1aa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Match	Length	ID	Description
1	64.5	22.8	132	4	US-09-149-476-362
2	58.5	20.7	573	4	US-09-134-001C-4480
3	56	19.8	359	1	US-08-153-848-24
4	56	19.8	359	3	US-09-299-843A-24
5	56	19.8	359	4	US-09-088-337B-24
6	56	19.8	359	5	PCT-US93-11153-24
7	56	19.8	378	3	US-09-299-843A-66
8	56	19.8	378	4	US-09-088-337B-66
9	56	19.8	472	4	US-09-108-020-12
10	55.5	19.6	554	4	US-08-180-371-2
11	55.5	19.6	554	5	PCT-US92-05707-2
12	52.5	18.6	1012	2	US-08-475-891A-4
13	52.5	18.6	1025	2	US-08-567-375-4
14	52.5	18.6	1025	2	US-08-587-680A-4
15	52	18.4	358	1	US-08-153-848-19
16	52	18.4	358	3	US-09-299-843A-19
17	52	18.4	358	4	US-09-088-337B-19
18	52	18.4	358	5	PCT-US93-11153-19
19	52	18.4	361	2	US-08-902-294-2
20	52	18.4	361	3	US-09-178-637-2
21	52	18.4	378	1	US-08-383-750-2
22	52	18.4	378	1	US-08-383-751A-2
23	52	18.4	378	3	US-08-153-848-15
24	52	18.4	378	1	US-08-352-678-2
25	52	18.4	378	3	US-09-299-843A-15
26	52	18.4	378	4	US-09-251-545-1
27	52	18.4	378	4	US-09-045-583-49

28	52	18.4	378	4	US-09-088-337B-15	Sequence 15, Appl
29	52	18.4	378	4	US-09-534-185-49	Sequence 49, Appl
30	52	18.4	378	5	PCT-US93-09636-2	Sequence 2, Appl
31	52	18.4	378	5	PCT-US93-11153-15	Sequence 15, Appl
32	52	18.4	410	1	US-08-153-848-7	Sequence 7, Appl
33	52	18.4	410	3	US-09-299-843A-7	Sequence 7, Appl
34	52	18.4	410	4	US-09-088-337B-7	Sequence 7, Appl
35	52	18.4	410	5	PCT-US93-11153-7	Sequence 7, Appl
36	51.5	18.2	3200	2	US-08-477-451-8	Sequence 8, Appl
37	51	18.0	415	4	US-09-198-956-6	Sequence 6, Appl
38	51	18.0	415	4	US-09-670-141-6	Sequence 6, Appl
39	51	18.0	422	4	US-09-025-580-3	Sequence 3, Appl
40	51	18.0	600	3	US-08-904-871-3	Sequence 3, Appl
41	51	18.0	1098	3	US-08-726-214-10	Sequence 10, Appl
42	51	18.0	1261	4	US-09-473-716-2	Sequence 2, Appl
43	51	18.0	2523	1	US-08-185-432-18	Sequence 18, Appl
44	51	18.0	2523	4	US-08-899-232-3	Sequence 3, Appl
45	51	18.0	2890	4	US-09-413-814-67	Sequence 67, Appl

## ALIGNMENTS

## RESULT 1

US-09-149-476-362  
; Sequence 362, Application US/09149476  
; Patent No. 6420526  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: 186 Human Secreted proteins  
; FILE REFERENCE: P2002P1  
; CURRENT APPLICATION NUMBER: US/09/149,476  
; CURRENT FILING DATE: 1998-09-08  
; EARLIER APPLICATION NUMBER: PCT/US98/04493  
; EARLIER FILING DATE: 1998-03-06  
; EARLIER APPLICATION NUMBER: 60/040,162  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/040,333  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/038,621  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/040,626  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/040,334  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/040,336  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/040,163  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/047,600  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,615  
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; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,502  
; EARLIER FILING DATE: 1997-05-23  
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; EARLIER APPLICATION NUMBER: 60/047,583  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,617  
; EARLIER FILING DATE: 1997-05-23  
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; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,503  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,592  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,581  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,584  
; EARLIER FILING DATE: 1997-05-23

[illegible]

OPERATING SYSTEM: PC-DOS/MS-DOS

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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX:
;
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 359 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-299-843A-24

Query Match 19.8%; Score 56; DB 3; Length 359;
Best Local Similarity 32.6%; Pred. No. 3.2;
Matches 14; Conservative 7; Mismatches 22; Indels 0; Gaps 0;

QY 4 CVRHVLGIGLVLKNIYFKHNSMYPSPKLSFQEAFLFFLLIL 46
Db 49 CFVGLLGNGLVILTYIFKRLKLTMTDTYLLNLAVADILFLIL 91

RESULT 5
PCT-US93-11153-24
; Sequence 24, Application US/09088337B
; Patent No. 6348574
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweikart, Vicki L.
; TITLE OF INVENTION: Novel Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/11153
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,452
; FILING DATE: 17-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Noland, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31794
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 359 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US93-11153-24

Query Match 19.8%; Score 56; DB 5; Length 359;
Best Local Similarity 32.6%; Pred. No. 3.2;
Matches 14; Conservative 7; Mismatches 22; Indels 0; Gaps 0;

QY 4 CVRHVLGIGLVLKNIYFKHNSMYPSPKLSFQEAFLFFLLIL 46
Db 49 CFVGLLGNGLVILTYIFKRLKLTMTDTYLLNLAVADILFLIL 91

RESULT 7
US-09-299-843A-66
; Sequence 66, Application US/09299843A
; Patent No. 6107475
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweikart, Vicki L.
; TITLE OF INVENTION: Novel Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/088,337B
; FILING DATE: 01-Jun-1998
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/153,848
; FILING DATE: 17-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6348574and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31794
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 359 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-088-337B-24

Query Match 19.8%; Score 56; DB 4; Length 359;
Best Local Similarity 32.6%; Pred. No. 3.2;
Matches 14; Conservative 7; Mismatches 22; Indels 0; Gaps 0;

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; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/299,843A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/088,337
; FILING DATE: 01-JUN-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/153,848
; FILING DATE: 17-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,452
; FILING DATE: 17-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Jill E. Uhl
; REGISTRATION NUMBER: 43,213
; REFERENCE/DOCKET NUMBER: 27866/32059B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX:
; INFORMATION FOR SEQ ID NO: 66:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 378 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-299-843A-66

Query Match 19.8%; Score 56; DB 3; Length 378;
Best Local Similarity 32.6%; Pred. No. 3.4;
Matches 14; Conservative 7; Mismatches 22; Indels 0; Gaps 0;

QY 4 CVRHVLGIGLVKLNLYFHKNMYPSPKLSFQFAFLFFLL 46
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Db 69 CFVGLGNGLVILTYIFKRLKMTDTYLLNLAVADILFLIL 111

RESULT 8
US-09-088-337B-66
; Sequence 66, Application US/09088337B
; Patent No. 6348574
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; Attorney: Schweikart, Vicki L.
; TITLE OF INVENTION: No. 6348574el Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/088,337B

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; FILING DATE: 01-JUN-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/153,848
; FILING DATE: 17-NOV-1993
; APPLICATION NUMBER: US 07/977,452
; FILING DATE: 17-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6348574and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31794
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 66:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 378 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-088-337B-66

Query Match 19.8%; Score 56; DB 4; Length 378;
Best Local Similarity 32.6%; Pred. No. 3.4;
Matches 14; Conservative 7; Mismatches 22; Indels 0; Gaps 0;

QY 4 CVRHVLGIGLVKLNLYFHKNMYPSPKLSFQFAFLFFLL 46
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Db 69 CFVGLGNGLVILTYIFKRLKMTDTYLLNLAVADILFLIL 111

RESULT 9
US-09-108-020-12
; Sequence 12, Application US/09108020A
; Patent No. 6143561
; GENERAL INFORMATION:
; APPLICANT: Randall, Douglas D.
; APPLICANT: Johnston, Mark L.
; APPLICANT: Miernyk, Jan A.
; APPLICANT: Luethy, Michael H.
; APPLICANT: Mooney, Brian P.
; TITLE OF INVENTION: USE OF DNA ENCODING PLASTID PYRUVATE DEHYDROGENASE AND
; TITLE OF INVENTION: BRANCHED CHAIN OXOACID DEHYDROGENASE COMPONENTS TO
; TITLE OF INVENTION: ENHANCE POLYHYDROXYALKANOATE BIOSYNTHESIS IN PLANTS
; FILE REFERENCE: UMO 1482
; CURRENT APPLICATION NUMBER: US/09/108,020A
; CURRENT FILING DATE: 1998-06-30
; EARLIER APPLICATION NUMBER: 60/051,291
; EARLIER FILING DATE: 1997-06-30
; EARLIER APPLICATION NUMBER: 60/055,255
; EARLIER FILING DATE: 1997-08-01
; EARLIER APPLICATION NUMBER: 60/076,544
; EARLIER FILING DATE: 1998-03-02
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 472
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; US-09-108-020-12

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Best Local Similarity 34.0%; Pred. No. 4.5;
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RESULT 10

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US-08-180-371-2  
; Sequence 2, Application US/08180371  
; Patent No. 6254861  
; GENERAL INFORMATION:  
; APPLICANT: Choudhury, Chandra  
; TITLE OF INVENTION: Hematopoietic Growth Factor Derived  
; TITLE OF INVENTION: from T Lymphocytes and Methods of Use Therefor  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
; ADDRESSEE: Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: United States of America  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/180,371  
; FILING DATE: 12-JAN-1994  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 906866  
; FILING DATE: 01 July 1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Gruber, Lewis S.  
; REGISTRATION NUMBER: 30,060  
; REFERENCE/DOCKET NUMBER: 27620/31668  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 474-6300  
; TELEFAX: (312) 474-0448  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 554 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-180-371-2  
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Best Local Similarity 26.0%; Pred. No. 6.4;  
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; Sequence 2, Application PC/TUS9205707  
; GENERAL INFORMATION:  
; APPLICANT: Choudhury, Chandra  
; TITLE OF INVENTION: Hematopoietic Growth Factor Derived from  
; TITLE OF INVENTION: T Lymphocytes and Methods of Use Therefor  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
; ADDRESSEE: Bicknell  
; STREET: Two First National Plaza, 20 South Clark  
; STREET: Street  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60603  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US92/05707  
; FILING DATE: 19920707  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Gruber, Lewis S.  
; REGISTRATION NUMBER: 30,060  
; REFERENCE/DOCKET NUMBER: 27620/30933  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 346-5750  
; TELEFAX: (312) 984-9740  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 554 amino acids  
; TYPE: AMINO ACID  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
PCT-US92-05707-2  
Query Match 19.6%; Score 55.5; DB 5; Length 554;  
Best Local Similarity 26.0%; Pred. No. 6.4;  
Matches 13; Conservative 13; Mismatches 15; Indels 9; Gaps 2;  
QY 14 IVLKNLYF-----HKNSMYPSPKLS--FOEAFLEFFFLILKNPLTLC 54  
Db 387 VPQNIWFVSHTSTLSTFEPLXXTPFKHYLXFCIVTSPSLCS 436  
RESULT 12  
US-08-475-891A-4  
; Sequence 4, Application US/08475891A  
; Patent No. 5859339  
; GENERAL INFORMATION:  
; APPLICANT: Ronald, Pamela C.  
; APPLICANT: Wang, Guo-Liang  
; APPLICANT: Song, Wen-Yuang  
; TITLE OF INVENTION: Procedures and Materials for Conferring  
; TITLE OF INVENTION: Disease Resistance in Plants  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
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; FILING DATE: 06-JUN-1995  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/373,375  
; FILING DATE: 17-JAN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bastian, Kevin L.  
; REGISTRATION NUMBER: 34,774  
; REFERENCE/DOCKET NUMBER: 02370-058910US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1012 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:



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Search completed: November 21, 2002, 13:43:12  
Job time : 16 secs

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: November 21, 2002, 13:40:47 ; Search time 35 Seconds  
(without alignments)  
205.587 Million cell updates/sec

Title: US-09-776-724A-142  
Perfect score: 283  
Sequence: 1 MRRVRHVLGIGLVLNLY.....PQEAFLFFLLKXNPLTLCSS 54

Scoring table: BLOSUM62  
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Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
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22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.\*  
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
283	100.0	54	20	AAV01442	Secreted protein e
73	25.8	85	22	ABBI7898	Human nervous syst
3	64.5	22.8	132	AAW74772	Human secreted pro
4	64	22.6	89	AAW96017	Human reproductive
5	64	22.6	89	AAW96695	Human reproductive
6	64	22.6	89	AAU18865	Novel prostate gla
7	64	22.6	89	AAU18919	Novel prostate gla
8	60	21.2	99	AAO06321	Human polypeptide
9	59.5	21.0	237	AAW47243	Arabidopsis thalia
10	59.5	21.0	251	AAW47242	Arabidopsis thalia

11	59.5	21.0	307	21	AAW47241	Arabidopsis thalia
12	59	20.8	310	22	AAU05132	Human odorant rece
13	59	20.8	310	22	AAW71441	Human olfactory re
14	59	20.8	310	22	AAW71472	Human olfactory re
15	59	20.8	310	23	AAU91543	Human PHO1-F5D6 a
16	59	20.8	339	22	AAW72954	Human olfactory re
17	58.5	20.7	611	20	AAW93594	O. longistaminata
18	58.5	20.7	673	23	ABF39635	Staphylococcus epi
19	57.5	20.3	70	23	ABP51925	Human colon specif
20	57	20.1	72	21	AAW15836	Arabidopsis thalia
21	57	20.1	94	21	AAW15835	Arabidopsis thalia
22	57	20.1	125	22	AAO07862	Human polypeptide
23	56.5	20.0	95	22	AAO07863	Human polypeptide
24	56.5	20.0	122	22	AAO03290	Human polypeptide
25	56	19.8	359	15	AAW53747	Seven transmembran
26	56	19.8	359	19	AAW48728	Murine V31 seven t
27	56	19.8	359	21	AAW21691	Murine 7TM recepto
28	56	19.8	359	23	AAU91233	Mouse 7 transmembr
29	56	19.8	378	21	AAW21699	7TM receptor prote
30	56	19.8	378	23	AAU91241	Mouse 7 transmembr
31	56	19.8	472	20	AAW88442	Arabidopsis branch
32	56	19.8	491	23	ABW47385	Listeria monocytog
33	55.5	19.6	103	22	AAO03045	Human polypeptide
34	55.5	19.6	134	22	AAO13437	Human polypeptide
35	55.5	19.6	172	23	ABW89059	Human polypeptide
36	55.5	19.6	554	14	AAW31930	Murine TC-CSF. Mu
37	55.5	19.6	554	14	AAW31932	Murine TC-CSF pept
38	55.5	19.6	554	22	AAE05133	Murine T cell-deri
39	55	19.4	59	22	AAW80894	Human haematologic
40	55	19.4	62	23	ABP00261	Human ORFX protein
41	55	19.4	199	22	AAU19189	Human G protein-co
42	54.5	19.3	200	21	AAW28190	Arabidopsis thalia
43	54.5	19.3	228	21	AAW28189	Arabidopsis thalia
44	54.5	19.3	312	21	AAW28188	Arabidopsis thalia
45	54.5	19.3	1757	20	AAW84351	Murine ubiquitin-p

## ALIGNMENTS

RESULT 1  
AAV01442  
ID AAV01442 standard; Protein; 54 AA.  
AC AAV01442;  
XX  
XX  
DT 18-MAY-1999 (first entry)  
XX  
DE Secreted protein encoded by gene 60 clone HOSDK95.  
XX  
KW Human; secreted protein; gene therapy; protein therapy; cancer; weight;  
KW tumour; chromosome mapping; forensic; haematological disease; allergy;  
KW inflammation; cell proliferation; viral infection; wound healing;  
KW modulation; appetite; behaviour; food additive; preservative.  
XX  
OS Homo sapiens.  
XX  
PN WO9903990-A1.  
XX  
XX 28-JAN-1999.  
XX  
XX 15-JUL-1998; 98WO-US14613.  
XX  
PR 18-AUG-1997; 97US-0056361.  
PR 16-JUL-1997; 97US-0052661.  
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PR 16-JUL-1997; 97US-0052874.  
PR 16-JUL-1997; 97US-0052875.  
PR 22-JUL-1997; 97US-0053440.  
PR 22-JUL-1997; 97US-0053441.

PR 22-JUL-1997; 97US-0053442.  
 PR 18-AUG-1997; 97US-0053683.  
 PR 18-AUG-1997; 97US-0055724.  
 PR 18-AUG-1997; 97US-0055725.  
 PR 18-AUG-1997; 97US-0055726.  
 PR 18-AUG-1997; 97US-0055946.  
 PR 18-AUG-1997; 97US-0055952.  
 PR 18-AUG-1997; 97US-0055985.  
 PR 18-AUG-1997; 97US-0055989.  
 PR 18-AUG-1997; 97US-0056359.  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 XX Duan R, Feng P, Ferrie AM, Florence KA, Fouad J;  
 PI Greene JM, Hu J, Ni J, Rosen CA, Ruben SM, Young PE;  
 PI Yu G;  
 XX  
 XX WPI: 1999-132234/11.  
 DR N-PSDB; AAX22270.  
 DR  
 XX  
 PT New nucleic acids encoding secreted human proteins - potentially  
 PT useful for treating and diagnosing diseases and identifying specific  
 PT binding agents  
 PT  
 XX  
 XX Claim 11; Page 233; 251pp; English.  
 XX  
 CC The invention relates to nucleic acid sequences (AAX22211 to AAX22282)  
 CC encoding human secreted proteins (AAY01383 to AAY01454). The secreted  
 CC protein gene sequences are deposited with the ATCC under deposit number  
 CC ATCC 209138, 209139 or 209141. Host cells containing vectors comprising  
 CC the nucleic acid sequences are used for the recombinant expression of  
 CC the secreted proteins. The polynucleotide and amino acid sequences are  
 CC useful for preventing, treating or ameliorating medical conditions e.g.  
 CC by protein or gene therapy. Pathological conditions can be also diagnosed  
 CC by determining the amount of the new polypeptides in a sample or by the  
 CC presence of mutations in the new polynucleotides. The nucleic acid  
 CC sequences, or its fragments, are useful for chromosome identification  
 CC and mapping; as antisense and triplex-forming therapeutics; in gene  
 CC therapy; for (forensic) identification of individuals; as molecular  
 CC weight markers; to identify related sequences or specific mRNA; in  
 CC preparation of oligomers and to raise anti-DNA antibodies. Antibodies are  
 CC useful as immunoassay reagents (including for in vivo imaging) and  
 CC therapeutically to inhibit or activate particular polypeptides. A very  
 CC wide range of disorders may be treated with the polynucleotide and  
 CC polypeptide sequences, e.g. autoimmune or haematological diseases,  
 CC allergy, inflammation, cancer or other forms of cell proliferation, viral  
 CC or other infections. The sequences may also be useful in wound healing,  
 CC to modulate differentiation of embryonic stem cells, to modulate weight,  
 CC appetite, behaviour etc. and as food additive or preservative. The  
 CC present sequence represents a human secreted protein (see descriptor  
 CC line for gene number and clone identification).  
 XX  
 SQ Sequence 54 AA;

Query Match 100.0%; Score 283; DB 20; Length 54;  
 Best Local Similarity 100.0%; Pred. No. 5.4e-34;  
 Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2  
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 ID ABB17898 standard; Protein; 85 AA.  
 XX  
 AC ABB17898;  
 XX  
 XX 23-JAN-2002 (first entry)  
 DT  
 XX  
 DE Human nervous system related polypeptide SEQ ID NO 6555.  
 XX

Human; nootropic; neuroprotective; cytostatic; dermatological; virucide;  
 immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;  
 antiparkinsonian; antickling; antianaemic; antiarthritic; cancer;  
 antirheumatic; hepatotropic; cerebroprotective; antinflammatory;  
 antiallergic; antidiabetic; antitumor; anticonvulsant; antifungal;  
 antiparasitic; cardiast; immune disorder; cardiovascular disorder;  
 neurological disease; infection; nephrotropic; gene therapy; vaccine.

OS Homo sapiens.

XX WO200159063-A2.

XX 16-AUG-2001.

XX 17-JAN-2001; 2001WO-US01334.

XX 31-JAN-2000; 2000US-0179065.

XX 04-FEB-2000; 2000US-0180628.

XX 24-FEB-2000; 2000US-0184664.

XX 02-MAR-2000; 2000US-0186350.

XX 16-MAR-2000; 2000US-0189874.

XX 17-MAR-2000; 2000US-0190076.

XX 18-APR-2000; 2000US-0198123.

XX 19-MAY-2000; 2000US-0205515.

XX 07-JUN-2000; 2000US-0209467.

XX 28-JUN-2000; 2000US-0214886.

XX 30-JUN-2000; 2000US-0215135.

XX 07-JUL-2000; 2000US-0216647.

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XX 23-AUG-2000; 2000US-0227009.

XX 30-AUG-2000; 2000US-0228924.

XX 01-SEP-2000; 2000US-0229287.

XX 01-SEP-2000; 2000US-0229343.

XX 01-SEP-2000; 2000US-0229344.

XX 01-SEP-2000; 2000US-0229345.

XX 05-SEP-2000; 2000US-0229509.

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XX 08-SEP-2000; 2000US-0231242.

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XX 12-SEP-2000; 2000US-0231968.

XX 14-SEP-2000; 2000US-0232397.

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XX 14-SEP-2000; 2000US-0232399.

XX 14-SEP-2000; 2000US-0232400.

XX 14-SEP-2000; 2000US-0232401.

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11-SEP-1998

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XX PF 06-MAR-1998; 98WO-US04493.
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PR 05-SEP-1997; 97US-0057669.
PR 05-SEP-1997; 97US-0057761.
PR 12-SEP-1997; 97US-0058785.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
PI Bednarik DP, Brewer LA, Carter KC, Duan R, Ebner R, Endress GA;
PI Feng P, Ferrie AM, Fischer CL, Florence KA, Greene JM, Hu JS;
PI Kiyaw H, Larleir DW, Li Y, Moore PA, Ni J, Olsen HS, Rosen CA;
PI Ruben SM, Shi Y, Soppet DR, Young PE, Yu GL, Zeng Z;
XX
DR WPI; 1998-506364/43.
DR N-PSDB; AAV59553.
XX
XX New isolated human genes and the secreted polypeptide(s) they encode
XX - useful for diagnosis and treatment of e.g. cancers, neurological
XX disorders, immune diseases, inflammation or blood disorders
XX
XX Claim 1; Page 564-565; 721pp; English.
XX
XX This sequence represents a secreted human protein encoded by the nucleic
XX acid molecule designated Gene 43 from the human cDNA clone HSNBB14
XX (deposited as clone ATCC 97899 and ATCC 209045).
XX The gene can be used to generate fusion proteins by linking to the gene
XX to a human immunoglobulin Fc portion (e.g. AAV59502) for increasing the
XX stability of the fused protein as compared to the human protein only.
XX The invention relates to 186 novel genes and their fragments (nucleic
XX acid sequences: AAV59511-V59812; amino acid sequences AAW4731-W75026)
XX which are useful for preventing, treating or ameliorating medical
XX conditions e.g. by protein or gene therapy. Also, pathological
XX conditions can be diagnosed by determining the amount of the new
XX polypeptides in a sample or by determining the presence of mutations in
XX the new polynucleotides. Specific uses are described for each of the 186
XX polynucleotides, based on which tissues they are most highly expressed in
XX (see AAV59511 for described uses).
XX
XX SQ Sequence 132 AA;
XX
XX Query Match 22.8%; Score 64.5; DB 19; Length 132;
XX Best Local Similarity 37.5%; Pred. No. 0.21;
XX Matches 21; Conservative 9; Mismatches 9; Indels 17; Gaps 5;
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XX | : | | | | | | | | | | | | | | | | | | | |
XX Db 1 MEHCLYVSHVGI-----NPYIHKNT-HFSINIYMWVDSQVNSFERFVPPFFLLI 49
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XX | : | | | | | | | | | | | | | | | | | | | |

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RESULT 4  
AAM96017  
ID AAM96017 standard; Protein; 89 AA.  
XX AC AAM96017;  
XX DT 21-NOV-2001 (first entry)  
XX DE Human reproductive system related antigen SEQ ID NO: 4675.  
XX KW Human; reproductive system related antigen; reproductive system disorder;  
KW cancer; gene therapy.  
XX OS Homo sapiens.  
XX PN WO200155320-A2.  
XX PD 02-AUG-2001.  
XX PF 17-JAN-2001; 2001WO-US01339.  
XX 31-JAN-2000; 2000US-0179065.  
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PR 24-FEB-2000; 2000US-0184664.  
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PR 17-NOV-2000; 2000US-0249299.  
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PR 01-DEC-2000; 2000US-0250160.  
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PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
PR (HUMA-) HUMAN GENOME SCI INC.
PR Rosen CA, Barash SC, Ruben SM;
PR WPI; 2001-465570/50.
PR N-PSDB; AAL01987.
PR Isolated nucleic acid molecule encoding a reproductive system antigen
PR is used in preventing, treating or ameliorating a medical condition -
PR Claim 11; SEQ ID NO 4675; 1297pp + Sequence Listing; English.
PR The present invention provides the protein and coding sequences of a
PR number of human reproductive system related antigens. These can be used
PR in the prevention and treatment of reproductive system disorders,
PR including cancer. The present sequence is a protein of the invention.
PR Sequence 89 AA;
PR Query Match 22.6%; Score 64; DB 22; Length 89;
PR Best Local Similarity 60.0%; Pred. No. 0.15;
PR Matches 12; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
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Db ||||: :| :|: |||:|
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AC AAM96695;
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DT 21-NOV-2001 (first entry)
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XX Human reproductive system related antigen SEQ ID NO: 5353.
DE Human; reproductive system related antigen; reproductive system disorder;
KW cancer; gene therapy.
XX Homo sapiens.
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XX 02-AUG-2001.
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 PR 08-DEC-2000; 2000US-0251869.  
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 PR 11-DEC-2000; 2000US-0251990.  
 PR 05-JAN-2001; 2001US-0259678.

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM;

WPI: 2001-476223/51.

N-PSDB; RAS30306.

Novel isolated prostate gland related polypeptide useful for diagnosis and treatment of disorders of prostate such as prostatodystonia, prostatosis, prostatitis, benign prostatic hypertrophy and malacoplakia

Claim 1; SEQ ID No 164; 512pp; English.

The invention relates to novel isolated prostate gland related nucleic acids (I) and polypeptides (II). (I) and (II) are useful for diagnosis, prognosis, prevention, and/or treatment of diseases and/or disorders of the prostate such as acute non-bacterial prostatitis, chronic non-bacterial prostatitis, acute bacterial prostatitis, prostatodystonia, prostatosis, granulomatous prostatitis, malacoplakia, benign prostatic hypertrophy or hyperplasia, and prostate neoplastic disorders, including adenocarcinomas, transitional cell carcinomas, ductal carcinomas, and squamous cell carcinomas. (I), (II) and antibody to (II) are useful for diagnosing and treating reproductive system disorders (Paget's disease), autoimmune disorders (systemic lupus erythematosus, rheumatoid arthritis), blood-related disorders (sickle cell anaemia), hyperproliferative disorders, urinary system disorders (glomerulonephritis), cardiovascular disorders (arrhythmias), respiratory disorders, musculoskeletal system disorders, neural activity and neurological disorders (Alzheimer's disease and Parkinson's disease), endocrine disorders (Addison's disease), gastrointestinal disorders (inflammatory disorders), liver disorders (biliary liver cirrhosis), pancreatic and gall bladder disorders, disorders of the large intestine, developmental and inherited disorders, diseases at the cellular level, and wound healing and epithelial cell proliferation. (I) or (II) is

Query Match 22.6%; Score 64; DB 22; Length 89;

Best Local Similarity 60.0%; Pred. No. 0.15;

Matches 12; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 13 LIVLKNLYFHKNMYPSPKL 32

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RESULT 7

Thu Nov 21 16:07:38 2002

**us-09-776-724a-142.rag**

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KW	osteopathic; prostate gland; prostatitis; adenocarcinoma; hair loss;	PR	14-SEP-2000;	2000US-0232400.
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KW	blood-related disorder; hyperproliferative disorder; respiratory;	PR	21-SEP-2000;	2000US-0234274.
KW	neurological disorder; endocrine disorder; inflammatory disorder;	PR	21-SEP-2000;	2000US-0234997.
KW	liver disorder; wound healing; food preservative.	PR	25-SEP-2000;	2000US-0234998.
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XX	WO200155447-A1.	PR	27-SEP-2000;	2000US-0235836.
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PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
PI
XX WPI; 2001-476223/51.
XX N-PSDB; AAS30360.
XX
XX Novel isolated prostate gland related polypeptide useful for diagnosis
PT and treatment of disorders of prostate such as prostatodystonia,
PT prostatosis, prostatitis, benign prostatic hypertrophy and malacoplakia
PT
XX
XX Claim 1; SEQ ID NO 218; 512pp; English.
XX
XX The invention relates to novel isolated prostate gland related nucleic
CC acids (I) and polypeptides (II). (I) and (II) are useful for diagnosis,
CC prognosis, prevention, and/or treatment of diseases and/or disorders of
CC the prostate such as acute non-bacterial prostatitis, chronic non-
CC bacterial prostatitis, acute bacterial prostatitis, prostatodystonia,
CC prostatosis, granulomatous prostatitis, malacoplakia, benign prostatic
CC hypertrophy or hyperplasia, and prostate neoplastic disorders, including
CC adenocarcinomas, transitional cell carcinomas, ductal carcinomas, and
CC squamous cell carcinomas. (I). (II) and antibody to (II) are useful for
CC diagnosing and treating reproductive system disorders (Paget's disease),
CC autoimmune disorders (systemic lupus erythematosus, rheumatoid
CC arthritis), blood-related disorders (sickle cell anaemia),
CC hyperproliferative disorders, urinary system disorders
CC (glomerulonephritis), cardiovascular disorders (arrhythmias),
CC respiratory disorders, musculoskeletal system disorders, neural activity
CC and neurological disorders (Alzheimer's disease and Parkinson's disease),
CC endocrine disorders (Addison's disease), gastrointestinal disorders
CC (inflammatory disorders), liver disorders (biliary liver cirrhosis),
CC pancreatic and gall bladder disorders, disorders of the large intestine,
CC developmental and inherited disorders, diseases at the cellular level,
CC and wound healing and epithelial cell proliferation. (I) or (II) is
XX
XX Query Match 22.6%; Score 64; DB 22; Length 89;
XX Best Local Similarity 60.0%; Pred. No. 0.15;
XX Matches 12; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
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XX AC AAC006321;
XX
XX DT 06-NOV-2001 (first entry)
XX
XX

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DE Human polypeptide SEQ ID NO 20213.
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XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorders; arthritis; inflammation.
XX
XX Homo sapiens.
XX
XX WO200164835-A2.
XX
XX 07-SEP-2001.
XX
XX 26-FEB-2001; 2001WO-US04927.
XX
XX 28-FEB-2000; 2000US-0515126.
XX
XX 18-MAY-2000; 2000US-0577409.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Drmanac RT;
PI
XX WPI; 2001-514838/56.
XX
XX N-PSDB; AAI86252.
XX
XX Isolated nucleic acids and polypeptides, useful for preventing
PT diagnosing and treating e.g. leukaemia, inflammation and immune
PT disorders.
XX
XX Claim 20; SEQ ID NO 20213; 1399pp + Sequence Listing; English.
XX
XX The invention relates to human polynucleotides (AAI79941-AAI93841) and
CC the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation.
XX
XX Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
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XX Best Local Similarity 41.7%; Pred. No. 0.67;
XX Matches 10; Conservative 7; Mismatches 7; Indels 0; Gaps 0;
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XX ID AAC47243 standard; Protein; 237 AA.
XX
XX AC AAC47243;
XX
XX DT 18-OCT-2000 (first entry)
XX
XX Arabidopsis thaliana protein fragment SEQ ID NO: 59523.
XX
XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
XX Arabidopsis thaliana.
XX

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PI Spytek KA, Li L;

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The present sequence is an olfactory receptor which is encoded by one of a number of novel polynucleotides. The polynucleotides can be used in screening for olfactory agonists and antagonists. The methods allow for the determination of primary scents and the identification of the odour receptors used to detect these primary scents. The methods also enable determination of secondary scents and the identification of combinations of odour receptors that are involved in detecting such secondary scents. This enables the construction of a scent representation (also called a scentfingerprint or scent profile), which may be used to

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